



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190795

TO: Ruixiang Li
Location: rem/4D59/4C70
Art Unit: 1646
Wednesday, May 31, 2006
Case Serial Number: 10/619992

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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78733

190795

M2

STIC-Biotech/ChemLib

From: Li, Ruixiang
Sent: Tuesday, May 23, 2006 9:19 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/619,992

Please do a standard search on:

SEQ ID NO: 2 against interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D59
Mail Box 4C70
(571) 272-0875

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2006, 12:48:33 ; Search time 35 Seconds
(without alignments)
2978.542 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215
Sequence: 1 MPVOAAQWTEFLSCPTCYNE.....MSKDNDPLKPVANGKMNVS 1191

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5-COMB pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6-COMB pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7-COMB pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H-COMB pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCRTUS-COMB pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE-COMB pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilled pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6215	100.0	1191	2	US-09-921-099A-2
2	6207	99.9	1191	2	US-09-921-099A-4
3	843	13.6	1048	2	US-09-921-099A-11
4	611	9.8	522	2	US-10-104-047-3665
5	194	3.1	2185	2	US-09-854-856-36
6	194	3.1	2185	2	US-10-010-720-36
7	194	3.1	2245	2	US-09-854-856-4
8	194	3.1	2245	2	US-10-010-720-4
9	194	3.1	2322	2	US-09-854-856-34
10	194	3.1	2322	2	US-10-010-720-34
11	194	3.1	2382	2	US-09-854-856-2
12	194	3.1	2382	2	US-10-010-720-2
13	193.5	3.1	1939	2	US-09-854-856-48
14	193.5	3.1	1939	2	US-10-010-720-48
15	193.5	3.1	1999	2	US-09-854-856-16
16	193.5	3.1	1999	2	US-10-010-720-16
17	193.5	3.1	2076	2	US-09-854-856-46
18	193.5	3.1	2076	2	US-10-010-720-46
19	193.5	3.1	2136	2	US-09-854-856-14
20	193.5	3.1	2136	2	US-10-010-720-14
21	193	3.1	1911	2	US-09-854-856-64
22	193	3.1	1911	2	US-10-010-720-64
23	193	3.1	1971	2	US-09-854-856-32
24	193	3.1	1971	2	US-10-010-720-32
25	193	3.1	2048	2	US-09-854-856-62
26	193	3.1	2048	2	US-10-010-720-62

27	193	3.1	2108	2	US-09-854-856-30	Sequence 30, Appl
28	193	3.1	2108	2	US-10-010-720-30	Sequence 30, Appl
29	193	3.1	2179	2	US-09-949-016-8129	Sequence 8129, Ap
30	189	3.0	1323	2	US-09-248-796A-19543	Sequence 19543, A
31	188	3.0	827	2	US-09-248-796A-17307	Sequence 17307, A
32	187	3.0	2157	2	US-09-854-856-52	Sequence 52, Appl
33	187	3.0	2157	2	US-10-010-720-52	Sequence 52, Appl
34	187	3.0	2217	2	US-09-854-856-20	Sequence 20, Appl
35	187	3.0	2217	2	US-10-010-720-20	Sequence 20, Appl
36	187	3.0	2294	2	US-09-854-856-50	Sequence 50, Appl
37	187	3.0	2294	2	US-10-010-720-50	Sequence 50, Appl
38	187	3.0	2354	2	US-09-854-856-18	Sequence 18, Appl
39	187	3.0	2354	2	US-10-010-720-18	Sequence 18, Appl
40	182.5	2.9	4019	2	US-09-854-133-425	Sequence 425, App
41	182	2.9	2004	2	US-09-854-856-58	Sequence 58, Appl
42	182	2.9	2004	2	US-10-010-720-58	Sequence 58, Appl
43	182	2.9	2032	2	US-09-854-856-42	Sequence 42, Appl
44	182	2.9	2032	2	US-10-010-720-42	Sequence 42, Appl
45	182	2.9	2064	2	US-09-854-856-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-09-921-099A-2
; Sequence 2, Application US/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Helfenfelder, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099A-2

Query Match 100.0%; Score 6215; DB 2; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPVOAAQWTEFLSCPTCYNEFPDENVHKPTISLGCSTHVCTCLNKLHKAACPPDQTAINMD	60
DB	1	MPVOAAQWTEFLSCPTCYNEFPDENVHKPTISLGCSTHVCTCLNKLHKAACPPDQTAINMD	60
QY	61	IVLPLVPFALLDLYGQVDPDHOSIKLSNGENKHYEVAKKVEDLALTYLKPSGGKGVAS	120
DB	61	IVLPLVPFALLDLYGQVDPDHOSIKLSNGENKHYEVAKKVEDLALTYLKPSGGKGVAS	120
QY	121	LNQSAISRMOVKRLVTVNCQVVEEGRVRAARASLIGERTVTELILOHNPQUSANL	180
DB	121	LNQSAISRMOVKRLVTVNCQVVEEGRVRAARASLIGERTVTELILOHNPQUSANL	180
QY	181	MAAVRARGQGFPGPAQOEALKLVLALDGSLSKRVLFLVQRLERFPQASTSIG	240
DB	181	MAAVRARGQGFPGPAQOEALKLVLALDGSLSKRVLFLVQRLERFPQASTSIG	240
QY	241	HVVQLLYRASCFKVTGRDESSIMQLEKFRSYEARLREHDAQIVHIAEAGLRISPEQW	300
DB	241	HVVQLLYRASCFKVTGRDESSIMQLEKFRSYEARLREHDAQIVHIAEAGLRISPEQW	300
QY	301	SSLIVGDLAKHSHMOSIIDKLOSPESFAKSVQELTIVLORTGDPANLRLPHELIANI	360
DB	301	SSLIVGDLAKHSHMOSIIDKLOSPESFAKSVQELTIVLORTGDPANLRLPHELIANI	360

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QY 361 DENPDVAVSPTWOLENAMAIVKTVVHGLVDFIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
DB 361 DENPDVAVSPTWOLENAMAIVKTVVHGLVDFIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
QY 421 OQGGCPRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNTVTTAGNVISVI 480
DB 421 OQGGCPRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNTVTTAGNVISVI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSSTSTLRALTEVKKVGVGANGONAAAPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISRSSTSTLRALTEVKKVGVGANGONAAAPSAD 540
QY 541 SYTENKIGSPKTPVSNVATAGSPSNVGTELSVPQKSSPFLTRPVYPVPHSENIQYRQ 600
DB 541 SYTENKIGSPKTPVSNVATAGSPSNVGTELSVPQKSSPFLTRPVYPVPHSENIQYRQ 600
QY 601 DPTQIPEFVPOYPOTGYVPPEPTVAGVAPCVPRFVRNNVPESSLPRASMPYADHYST 660
DB 601 DPTQIPEFVPOYPOTGYVPPEPTVAGVAPCVPRFVRNNVPESSLPRASMPYADHYST 660
QY 661 FSPDRMNSSPYQPPPOYPGPVPVPSGMVAVYVDSRRIWRPMTQRDDIIRSNLSPM 720
DB 661 FSPDRMNSSPYQPPPOYPGPVPVPSGMVAVYVDSRRIWRPMTQRDDIIRSNLSPM 720
QY 721 DVHSSVYQTSLRERNSLDGYYSVACOPSPSEPTVPLPREPCGHLKTSCEQIRKPD 780
DB 721 DVHSSVYQTSLRERNSLDGYYSVACOPSPSEPTVPLPREPCGHLKTSCEQIRKPD 780
QY 781 QMAQYHTOKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
DB 781 QMAQYHTOKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
QY 841 CGTIGSCINAIIDSEPKDVIANNAVLMDLDSGVKRVHLFETQRKTEEDPIIPPSDGP 900
DB 841 CGTIGSCINAIIDSEPKDVIANNAVLMDLDSGVKRVHLFETQRKTEEDPIIPPSDGP 900
QY 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRWSYGNBATS 960
DB 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRWSYGNBATS 960
QY 961 SAHYERDRPIYVTDLSGHRKHSSTGDLISLELOAKSNLILQREANALAMQOKMSLDB 1020
DB 961 SAHYERDRPIYVTDLSGHRKHSSTGDLISLELOAKSNLILQREANALAMQOKMSLDB 1020
QY 1021 GSHLTNLNLKSELNKGELSDYTEDADTKPDRIELELSALDDBEPGQSEPIBELI 1080
DB 1021 GSHLTNLNLKSELNKGELSDYTEDADTKPDRIELELSALDDBEPGQSEPIBELI 1080
QY 1081 DIQLGISSONDQILNMAVENGHVVOOHOKEPKOKKOSLGEDHVLLEBQKTLIPVTSQF 1140
DB 1081 DIQLGISSONDQILNMAVENGHVVOOHOKEPKOKKOSLGEDHVLLEBQKTLIPVTSQF 1140
QY 1141 SQPLPVISINASCPIPTTSVSAGNLILKTHVMSKXNDPLKPVANGKMNVS 1191
DB 1141 SQPLPVISINASCPIPTTSVSAGNLILKTHVMSKXNDPLKPVANGKMNVS 1191

RESULT 2
US-09-921-099A-4
; Sequence 4, Application US/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

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; LENGTH: 1191
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-921-099A-4
Query Match 99.9%; Score 6207; DB 2; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVOAAQWTEFLSCLPCVNEPDENVHKPISLCSHTVCKCLNKHAKACPPDQTAIND 60
DB 1 MAVQAQWTEFLSCLPCVNEPDENVHKPISLCSHTVCKCLNKHAKACPPDQTAIND 60
QY 61 IDVLVYNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKVEDLALYLKPSGGKGVAS 120
DB 61 IDVLVYNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKVEDLALYLKPSGGKGVAS 120
QY 121 LMQSALSRPMQRKLVTLVNCQLVEEGRVRAARAARSLGERVTTELILQHONPOQLSANL 180
DB 121 LMQSALSRPMQRKLVTLVNCQLVEEGRVRAARAARSLGERVTTELILQHONPOQLSANL 180
QY 181 MAAVRARGCQFLGPAQOEALKVLVLALEDGALSRLKVLVLFVQRLERFPQASTSIG 240
DB 181 MAAVRARGCQFLGPAQOEALKVLVLALEDGALSRLKVLVLFVQRLERFPQASTSIG 240
QY 241 HVVOLLYRASCFKVTYKRDSDSLMOLKEBFRRSYEARLREHDAQIVHIAEAGLRISPEQM 300
DB 241 HVVOLLYRASCFKVTYKRDSDSLMOLKEBFRRSYEARLREHDAQIVHIAEAGLRISPEQM 300
QY 301 SSLVYGDILAHKSHMOSIIDKQSPESFAKSVQELTIVLORTGDPANLRLPHLELLANI 360
DB 301 SSLVYGDILAHKSHMOSIIDKQSPESFAKSVQELTIVLORTGDPANLRLPHLELLANI 360
QY 361 DENPDVAVSPTWOLENAMAIVKTVVHGLVDFIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
DB 361 DENPDVAVSPTWOLENAMAIVKTVVHGLVDFIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
QY 421 OQGGCPRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNTVTTAGNVISVI 480
DB 421 OQGGCPRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNTVTTAGNVISVI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSSTSTLRALTEVKKVGVGANGONAAAPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISRSSTSTLRALTEVKKVGVGANGONAAAPSAD 540
QY 541 SYTENKIGSPKTPVSNVATAGSPSNVGTELSVPQKSSPFLTRPVYPVPHSENIQYRQ 600
DB 541 SYTENKIGSPKTPVSNVATAGSPSNVGTELSVPQKSSPFLTRPVYPVPHSENIQYRQ 600
QY 601 DPTQIPEFVPOYPOTGYVPPEPTVAGVAPCVPRFVRNNVPESSLPRASMPYADHYST 660
DB 601 DPTQIPEFVPOYPOTGYVPPEPTVAGVAPCVPRFVRNNVPESSLPRASMPYADHYST 660
QY 661 FSPDRMNSSPYQPPPOYPGPVPVPSGMVAVYVDSRRIWRPMTQRDDIIRSNLSPM 720
DB 661 FSPDRMNSSPYQPPPOYPGPVPVPSGMVAVYVDSRRIWRPMTQRDDIIRSNLSPM 720
QY 721 DVHSSVYQTSLRERNSLDGYYSVACOPSPSEPTVPLPREPCGHLKTSCEQIRKPD 780
DB 721 DVHSSVYQTSLRERNSLDGYYSVACOPSPSEPTVPLPREPCGHLKTSCEQIRKPD 780
QY 781 QMAQYHTOKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
DB 781 QMAQYHTOKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
QY 841 CGTIGSCINAIIDSEPKDVIANNAVLMDLDSGVKRVHLFETQRKTEEDPIIPPSDGP 900
DB 841 CGTIGSCINAIIDSEPKDVIANNAVLMDLDSGVKRVHLFETQRKTEEDPIIPPSDGP 900
QY 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRWSYGNBATS 960
DB 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRWSYGNBATS 960

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QY 961 SAHYVERDFITVULSGHRKHSSTGDLLELOQAASNSLLQREANALAMQKMSLSE 1020
DB 961 SAHYVERDFITVULSGHRKHSSTGDLLELOQAASNSLLQREANALAMQKMSLSE 1020
QY 1021 GHRLTLNLISKEIELENGELQSDYEDATDTPKDRDIELELSALDTEPDSGSEPIEELI 1080
DB 1021 GHRLTLNLISKEIELENGELQSDYEDATDTPKDRDIELELSALDTEPDSGSEPIEELI 1080
QY 1081 DIQLGISNDOLLNGMAVENGHVVOOHQKEPPKQKQSLGEDHVLLEQKTLTPVTSCEP 1140
DB 1081 DIQLGISNDOLLNGMAVENGHVVOOHQKEPPKQKQSLGEDHVLLEQKTLTPVTSCEP 1140
QY 1141 SQPLPVSISNASCLPTTTSVSAGNLLKTHVMSSEDKNDPLKPVANKMNS 1191
DB 1141 SQPLPVSISNASCLPTTTSVSAGNLLKTHVMSSEDKNDPLKPVANKMNS 1191

RESULT 3
US-09-921-099A-11
/ Sequence 11, Application US/09921099A
/ Patent No. 6602707
/ GENERAL INFORMATION:
/ APPLICANT: Hefeneider, Steven
/ APPLICANT: Merkins, Louise
/ APPLICANT: Bennett, Robert
/ APPLICANT: Seiss, Donald
/ TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
/ FILE REFERENCE: 00-617-A
/ CURRENT APPLICATION NUMBER: US/09/921,099A
/ CURRENT FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 11
/ LENGTH: 1048
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-09-921-099A-11

Query Match 13.6%; Score 843; DB 2; Length 1048;
Best Local Similarity 30.6%; Pred. No. 4,3e-59;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

QY 4 QAOWTEFLSCPTCYNEPDENHAKPISLGSHTVCTCLNKLHR--KACPPDQTANTDOI 61
DB 6 QGGQWQEVCCSICNHNENE-TFLPVSLICGHVTCCKAKEPENQTKPCPHDWMKTTSP 64
QY 62 DVLPVNFALLQVGAQVPHQSIKLSNLGENKHVEYAKKCVEDLALYLKPLSGKGVASL 121
DB 65 SEYPPNNVALLSVI---FPRKQCMTSLGAVNSEAKRYDQLSIQ-TAKFPREADSERG-GTV 119
QY 122 NQSALSRPMQOKLVTLVNCQVVEEGRVAMRAARSLGERTVTELLLOHQNPOOLSANLM 181
DB 120 SSREISRTLOKRVKALLCYQWREVDRLKTLKMCGRISERVMIEILISQSTHVSQJW 179
QY 182 AAVRARGCOFLPAMOEALKLVLLALDEGSAISRVLYLVFQVRLPERFPQASKTSIGH 241
DB 180 SAVRARGCOFLPAMODVLRLLMLTLETGECTARKNLVMYVOTIASDYPOVSKTCVGH 239
QY 242 VVQLLYRASCFCFKTKKDEDSLMQLKEEPRSYEAREREDAOIVHAMEAGLRISPEQMS 301
DB 240 VVQLLYRASCFCVNLKRDGESSLMQLKEEPRSYEAREREDAOIVHAMEAGLRISPEQMS 299
QY 302 SLIYGDLAHSHMOSIIDKLQSPESFAKSVQELTIVLQRTGDPAN-----LNRLRP 352
DB 300 ALLYVADQSHRSHMOSIIDKLQSGNSYQCGVEELRAL---AGSQTMLVAYRYFLTVQVLP 356
QY 353 HELLANTIDPNDAVPTMEOLEMANVAVKTVHGVLDPIQNV---SRGHEPRQOPQMS 409
DB 357 CLEFFRGIHEDTSMIGDALHQLIRILK--LHSGODDLRKMPKEERKGVILLQAEVPGG 414
QY 410 KYKTSKRDLDQOQGGCPRGTCNCTFAHSHOBELEKYRLRNKNINATVTFPLNKKVGNNTV 469
DB 415 -----MGGPGGSG-----GAEAGRI----- 430

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QY 470 TTAGNVISVIGSTETTGKIVPSTNGISNNSVSQLISRSTDSITLRALETYKVKVGA 529
DB 431 ----GGLHPLYSQIDETGSRISRTNPKDSSHNSPQ----- 461
QY 530 NGQNAAGPSADSVTENKISPPKTPVSNVAATSAGPSNVGTELNSVQKSPPLTRVPVY 589
DB 462 -----TPPKQRPQKRYQMGIPPNRNG-----YSSDAPPIIPSHQOQ 497
QY 590 PPHSENIQYQDPRTQIPEVPOQYPPPTVPAGVACVPRFVSNVNESSLPP 649
DB 498 PPP-----QEFNS--QHLPQRFGRGQRGAAPPBPQP-----MPLIGVD-----MFG 539
QY 650 ASMPYADHSTSPRDRMNSP-----YQPPRPQPIGPVPVPSGMYAAYVDSRIWRP 704
DB 540 APPMQATEVLT-ADQGMVNGTPQRVVIMQSPFHLPGGPVVMIPQOQWPPPOSMTPEVGP 598
QY 705 MYQRDDIIRNSNLPMPDVHSSV-YQTSLERRYNSLDGYSV---ACOPPEPRRTV 757
DB 599 M-----GFMGPMTPSIPVQVPPNTMTATSPGSIYIYPAASFPQGPPTI 643

RESULT 4
US-10-104-047-3665
/ Sequence 3665, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTYTUTE
/ TITLE OF INVENTION: No. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3665
/ LENGTH: 522
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match 9.8%; Score 611; DB 2; Length 522;
Best Local Similarity 34.1%; Pred. No. 1e-40;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YTPPPTVAGVAPCVPRFVRSNVPESSLPASMPYADHYSTFSPRDRMNSPYQPP 677
DB 2 YTPPP-----QCYSRFVR---PPSAPBPAPYLDHYRPLY-QERVANSQYGTQRP 49
QY 678 QPYGPVPVPSGMYAVPVYDSRIWRPMYQRDDIIRNSLPPMDVHSSV--YQTSLERR 735
DB 50 Q-----YPPI-----YPSHYDGRVYPAFSYTRREIFRESPI-DLEIPPAVPSVPSRER 100
QY 736 YNSLDGYVYACQ-----PS-----BPRTYPLPRECGHLKTKSCQEQIRKQDQMYQNH 787
DB 101 YQIISYVPAHPQIRPSYVREPPYSRLPPQP---HPSLDLHRRKREIMQLEB 156
QY 788 QKAPLVSTPLPATOSPTPPSPFLFSVDFRADSESVSGTKFEEDHLSHPMSCGTIGSC 847
DB 157 RK---VISPPPPA-PSPTLP-PTFHHEEFLDDDLKAVG-KYKGNDSQSPMSCDITGSY 210
QY 848 INADSEPKDVANSNAVIMDLDSGDVKRRVHLFETQRTKE--EDPIIPFSDGPIISKW 905
DB 211 IGTKDAKPPDVVAAGSVEMANNYESKGM--RDQRLDQRAAETSDDDLIPFGDRPTVSRF 268
QY 906 GAISRSRPGYHTTPOVQATASQSAIKPISVDVYVYNAVDSRW--SSYG--NEATSS 961
DB 269 GAISRTSKITYGAGBPQAMAPQGAFTKINSIDSPI--GTHGNGASPIYSHQNIIPQO 326
QY 962 AHYVERDFITVULSGHRK--HSSTGDLLELOQ-----AKNSLLQ 1004
DB 327 GHFERERISMESVASHGKPLPSAREQRLLELOQNHQISOOTQLRGPEAVSNRLVLQ 386

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; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/010,720
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 2185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2185)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-36

Query Match          3.1%; Score 194; DB 2; Length 2185;
Best Local Similarity 18.5%; Pred. No. 1e-05;
Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

QY 48 KACPQDAINT-----DIDVLFNFAIIQVGAQVPHQSIKLSNLGEN 92
DB 315 KRASFVSIQTPFEMAPMEYEKYDESDVYAFGCMLEMAISEYF----- 361
QY 93 KHYEVAKKVEDDALYKLGSGKVASLNSAL-----SRPMOKLVTLVN 139
DB 362 ----VSECQNAQIYRRTYSGVK-PASFDKVAIPVKEIIEGCRKONDERYSIDOLN 415
QY 140 COLVEEGVRAMRAARSIGERTVELLIHQNPOLSAIAMAARAGCOFLGPMQOE 199
DB 416 HAFQGETGVRLAEEDDEGKAIKLMFRIEDIKLK-----GKKQME 460
QY 200 ALKLVLLAEDGSALSRYLVLFVQRLPRPQASKISGHVQVLLYRASCFTVKRDE 259
DB 461 AIEF-----SFDLERDVEDVAQEMVEGVCEDGHTMAKAIKDR-- 501
QY 260 DSIWQKEEPRSYEARREHDAQIVHIMEAGLRISPEWMSLYLXGDLAKHSHMOSIID 319
DB 502 -VSLIKRKEQR-QLVREEQEK-----KOEBSLKOQVEGSSASQGIK 544
QY 320 KLOSPEFAKSVQELTIVLORTGDP-----ANLNRRLPHLELLANTDPNDVSPTW 371
DB 545 QLPASSTGIPFASSTASVSTQVEBEPBADOHQLOQYQPSISVLS--DGVDSGQSS 602
QY 372 EOLENMAVAKTVVHGLVDFIONYSRKGHET-----PQOPNSKYKTSMCRDL 419
DB 603 VFTESVSSQCTVSYG-----SQHEQASHSTGVPHIPSTVOAQSPGHVPPSSVAQ 656
QY 420 RQGGGCRRTNCTFASQOELEKRYLRANKKINATVTFPLMKVGNNTVTAGVIVS 479
DB 657 QSQGQ-PSSSSLGVSSSQITQHPQ-----QQGQIQTAHPQ----- 692
QY 480 IGSTETTGKIVSTINGISNAENSVSOLISRSSTDSTLRALETYKVKVKGANGAAGPSA 539
DB 693 -----QTVQYSLSQ-TSTSSSEAT-----TQPVSQPQA 719
QY 540 DSVTEKIGSPKPTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRY-----PVYPP 591
DB 720 PQVLP-QVAGAKQLPVSQVPRTIQGEPOIPIVATQPSVNVHNSGAFPLPVGOPLPTLP- 777
QY 592 HSENIQVQDPRPTQIFEEVPOV--PQTGYRPPRTPVAGVAPCVRFVANSNNPESSLP- 648
DB 778 -----QYVSQLPISIPHVSTADTGFSSLPITMAAGITQ--PLTLTASSATTATIG 827
QY 649 -----PASPMPYADHVTSPFRDMNSSPY-----QPPP-----PQPYGPVPVPSGMYAPV 694
DB 828 VSTVVSQGP-----TLQPVTLQPLSQVHPQLQLQPVQSGVGRANLGAABEVLSSGDVL 882

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QY 695 YDSKRIWRPMPYQRDDIITSNLSIPMDVHSSVYQTSLEERYNSLDGYYSVACQPPSEPR 754
DB 883 YQGFPRRLPPQYFGSNTLAPSSNVASVCHSTVTLXPRMTEVLATGPFTVVQPVESN 942
QY 755 TTVPL-----PREPCGL-----KTSCEQIRRKRPDQMAQYHTOKAPLVSTLTPVATQ 802
DB 943 LVPVKGVGQVQVQSPGSLAQAPTTSSQAVLES-----TQGVQVAPAEVAVVA 994
QY 803 SP--TTPSPL-FSVDF-----RADFSESVSGTKFEBDHLSHVSPMSCGTTGICINAI 851
DB 995 QVQATQPTTLASSVDSADHDVASGMSDGNENVPSSSGRHEGRTTKRHYKSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNAYLMDLSDGVYRRNHLFETQRTKTEEDPIIFPSQPIISKMG 906
DB 1055 TSPPKRLILNNSKGDVVECOLETHNRKMTFKFDLGDNDPEIATIVNDFIL---- 1110
QY 907 AISRSS-----RTGYHTDPVQA-----TASQ--GSATKP 934
DB 1111 AIERESFVQVQVEIIEKADBLEMSDEVSVPEBDQGLESLQKDDYGFSGSQKLEGEFKP 1170
QY 935 ISVSDVVPYVNAVDSRWSSYGNBATSSAHYVERDRPIVTDLSGHRHSS--TGDLI-SL 990
DB 1171 PASSWPQIGIPTS-----SLTQVVAJAGR-REIVGVPDESRLRESKVFPSEITDTV 1222
QY 991 ELQAKSNLSLLQREANALAMQOKNSLDRGHLITNLKSEIELANGELQSDYTEDAD 1050
DB 1223 AASTAQSPQMNLSHSSASLSLQAFS-----ELRRQM--TGCPMT 1261
QY 1051 TKPRDR-----IELESLADTIDPEPDGSEPIEELND--IQLGISQNDQ 1092
DB 1262 APPNPSHTPTFPVVPFPLSSIAGVPTTAAATPAPVATSPFDISTSVIQSIVYPTPEE 1321
QY 1093 LUNGMAVENGHVQHQKPPROKQSLGBDHVILEQKITLIPVTSFSGOPLVPVISNAS 1152
DB 1322 GIAGVATSTGVVTSGLPIRP-----VESPVLSVSVSITPAPVISTTS 1368
QY 1153 -CLPITTSVS 1161
DB 1369 PSLQVPTSTS 1378

RESULT 7
US-09-854-856-4
; Sequence 4, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US-0178-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2245)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-4

Query Match          3.1%; Score 194; DB 2; Length 2245;
Best Local Similarity 18.5%; Pred. No. 1.e-05;
Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

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QY 48 KACPEDQTAINT-----DIDVL.PVNFAIIQLVGAQVPHDQSTIKLSNLGEN 92
Db 375 KRASFAXSVIGPPEFMARPEMVEEKYDESVDVYAFGCMLEMAATSEYP-----421
QY 93 KHVEYAKKCVEDIALYLKPLSGKGVAJLNOGAL-----SRPMQRKVLTVN 139
Db 422 -----YSECONNAQIYRRTSGVK--PASFDKVAIPEVKEIIEGCIKRONDERYSIKDLN 475
QY 140 COLVEEGRVAMRAARSIGERTVTELLIOHONPOOLSANLMAAARAGCQFLGPMQOE 199
Db 476 HAFPOETGVREVLAEEDDEGEKAIKLMWRIEDIKLK-----GKYKDE 520
QY 200 ALKVLVLALEDGSAISRKVLVL.FVVORLEPRPQASKTSGHVVOLLYPASCFTKRD 259
Db 521 ATEP-----SFDLERDVPEDVAQEMVSGYVCEGDHKTMAKAIKDR--561
QY 260 DSSLMOQLKEEFSYEALREHDAQIVHIMEAGLRI.SPEWSSLLYGLDAHKSHMQSIID 319
Db 562 -VSLIKRKEOR--QVREEOEKK-----KQESSLKOQVEQSSASQTGIK 604
QY 320 KLOPSSPAKSVQELTYLQRTGDP-----ANLNRLRPHLELLANIDPNDAVSPW 371
Db 605 QLPASASTGIP.TASTTSASVSTOVEPEEPADQHOQLQOQPSISVLS--DGTVDSCQSS 662
QY 372 EQLENAMVAVKTVVHGLVDFIONYSRKGHET-----POQOPNSKYKTMCRDL 419
Db 663 VTEBESVSCQIVSYG-----SQHEQANSTGVPCHITSTVOAOSQPGVPPSSVAQG 716
QY 420 ROOGGCPRGCTNCTFAHSGELEKYLRLNKNKINATVPFLNKVGVNNTVTTAGNVISV 479
Db 717 QOQOQ--PSSSSLTGVSSQPIQHPQ-----QOQGIQOTAPQ-----752
QY 480 ISTETTKIVSTNGCISNAENSVSQILSRDSTILRALEYKVKVKGANQONMAQSPA 539
Db 753 -----QTVQYSLSQ--TSTSEAT-----TAQVPSQQA 779
QY 540 DSVTENKIGSPKPTPVSNVATSAAGSN--VGTSLMSVPOKSPFLTRV-----PVYPP 591
Db 780 PQLVP--QVAGAKOLPISQVPTPIQSEPOQVPVATQEPVNVVHSGANHLPGQPLPTLLP- 837
QY 592 HSENIQYFODPRTQIPEFVPOY--PQTGYYPPTPVPAVAPCPVPRVSNVPESSLP- 648
Db 838 -----QVPSQIPSTPHVSTAQTGFSPLITMAAGITQ--PLTLASSATTAIRG 887
QY 649 -----PASMPPYADHVSFTSPBRDMNSPY-----QPP-----PQYGPVPPVSGMAYAV 694
Db 888 VSTVPSOLP-----TLQPVYQLPISQVHPQLLQPAVQSGMGPANLGOAAEVLSSGDLV 942
QY 695 YDSRRIWRPMPYQORDIIRSNLSLPPMDVMHSSVYQTSLEERYNSLDGYYSVACQPPSEPR 754
Db 943 YQGFPRRLPQYRGDGNIAPISSNVASVCHSTYLAXPMPTVULATGCIPTTVQPIVESN 1002
QY 755 TVVPL-----PREPCGHL-----KTSCEBOIRRRPDQMAOYHTQKAPLVSTLPAVATQ 802
Db 1003 LLYVPMGVGQVQVQSGPGLAQAPTTSSQOAVLES-----TQGVSOVABAEVAVAA 1054
QY 803 SP--TPSPSL-PSVDP-----RADFSHSVGTFFEDHLSHPMSGTTIGSCINAI 851
Db 1055 QOPATOPPTLASSVDASHDVASGMSDGMENVPSSGRHEGRTTKHRYKSVASRSRHEK 1114
QY 852 DSEPKQVIAN-----SNAVILMDLSDGVKRRVHLFETQRTKEEDLIPSPDPIISKMG 906
Db 1115 TSPFKILRLNVSXKGRVVECOLETHNRKRVTKFKDLGDNPBEIATIMNNDFIL-----1170
QY 907 AISRSS-----RTGYHTDPVQA-----TASQ-----GSATKP 934
Db 1171 ATERBESFVQVARETIKADMLSEDSVSEPEBDQGLSLOKXODYGFSGSQKLEGEKQ 1230
QY 935 ISVSDVVPVYNAVDSKMSYGNATSSAHYVERDRILVLDLSGRHSS--TGDL--SL 990
Db 1231 IPASSMPOOIGIPTS-----SLTGVHSGR-RFIVSVPEBSRLRESKVPSEITDTV 1282

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QY 991 ELQAKSNLSLLQREANALAMQOKNNSLDEGRHLTLNLISKEIELRNGELQSDYEDATD 1050
Db 1283 AASTQSGMNLSSHASBSLSQAFS-----ELRRQM-----TEGPNT 1321
QY 1051 TKPRD-----IELESLDITDEPDGQSEPIEELD--IQGISQNDQ 1092
Db 1322 APPNFSHTGPRPPVPPFLSSJAGVPTTAAAPVAPATSSPNDISTSVTQSEVTVPTBE 1381
QY 1093 LUNGMAVENGHVQHQKPEPKQKQSLGEDHVILEBOKTILPTSCFQPLPVISNNS 1152
Db 1382 GIAGVATSTGVTTSGGLPIPP-----VSESPVLSVSSITTPAVVISSTIS 1428
QY 1153 -CLPITTSVS 1161
Db 1429 PSLQVPTST 1438

RESULT 8
US-10-010-720-4
; Sequence 4, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: Beltrandelrio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/010, 720
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: US 60/206, 015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854, 856
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2245
; TYPE: PR
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(2245)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-4

Query Match 3.1%; Score 194; DB 2; Length 2245;
Best Local Similarity 18.5%; Pred. No. 1,1e-05;
Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

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QY 649 -----PAMPYADHYSTSPDRMNSPY-----OPP-----POPYGPVPVPSGMYAV 694
DB 828 VSTVPSQLP-----TLQPTVQLPSQVHPQLQPAVSGMGPANLQGAAPVPLSSGDL 882
QY 695 YDSRRIMRPMYQORDIIRSNLPPMDVHSSVYQTSLEERYNSLDGYVAVACQPPSEPR 754
DB 883 YQGFPRRLPPQYPGSNNIAPSSNVASVCHISTYLAKPMPTEVLATPGVPTVQPVESN 942
QY 755 TTVPL-----PREPGHL-----KTSCEBOIRRRKPDQMAOYHTQKAPLVSTLPVATQ 802
DB 943 LVPVPGVGQVQVQVSGSLAQAPTTSSQAVLES-----TQGVQVAPAEVAVAA 994
QY 803 SP--TPSPPL-PSVDF-----RADFSESVSGTFEBEDHLSHYSPMCGTIGSCINAI 851
DB 995 QPQATOPTTLASSVDVAHSDVAGMDSGDNENVPSSSGRHEGRTTKRHYKSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNAVLMDLDSGDVKKRVHLEFETQRTKEEDPIIPSPGPIISKWG 906
DB 1055 TSRPKRLIINVSNGKGRVVECOLETHNRKMVTFFKFDLDGDNPEIATIMVNDPFI----- 1110
QY 907 AISRBS-----RTGYHTTDPVQA-----TASQ-----GSATKP 934
DB 1111 ATERSEFVDQVREIIEKADEMLSDEVSVREBDOGLSLOQKDYGFSGSOKLEGEFKOP 1170
QY 935 ISVSDYVPVYNAVDSRWSYSGNEATSSAHYVERDFIYTLDSGHRGHS---TGDLL-SL 990
DB 1171 IPASSMPQOIGIPTS-----SLTQVHVSAGR-RITVAPVESRRLRESKVPFSEITDIV 1222
QY 991 ELQQAQNSLLIQRANALAMQOKNSLDEGRHLTLNLISKELELNGELQSDYTEARD 1050
DB 1223 AASTQSPGMNLSHSASLSLOQAFS-----ELRRQM-----TEGPNT 1261
QY 1051 TAPDDB-----IELESLALDDEPDGSEPIEILID--IOLGISSQNDQ 1092
DB 1262 APPNHSHTPTTPVVPFSLSIAGVPTTAATPVPATSPPDISTSYIQSVYVPTPE 1321
QY 1093 LINGMAVENGHVPOHQEKPPKOKSLGEBHVILEBQKTIIPVTSFSGOPLPVSIANS 1152
DB 1322 GIAGVATIGVATVSGGLPIFP-----VESPVLSVSVSITIPAVVSIISTS 1368
QY 1153 -CLPITTSVS 1161
DB 1369 PSLQVPTSTS 1378

RESULT 10
US-10-010-720-34
; Sequence 34, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Slichtehorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same, And Uses Thereof
; FILE REFERENCE: Lex-0382-USA
; CURRENT APPLICATION NUMBER: US/10/010,720
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 2322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: VARIANT
; LOCATION: (1)....(2322)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-34

Query Match      3.1%; Score 194; DB 2; Length 2322;
Best Local Similarity 18.5%; Pred. No. 1.1e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

QY 48 KACPFDQTAINT-----DIDVLPVNFALLQVGAQVPHQSIKLSNLGEN 92
DB 315 KRASPAKSVTGPPEPMABPMYEEKYDESVDVAFKCMHBMATSEYP----- 361
QY 93 KHYEAKKCEVEDIALYLPKLSGKGVAASINQSL-----SRPMQRKVLTVN 139
DB 362 -----YSBQNAQAQYRRVATSGVK--PASFDKVAIPEVKIIEGCIIRONDERYSIIDLN 415
QY 140 COLVEEGRVAMRAARSLGERTVTELLIQHONPQOLSANLMAAVRAGCQVLGRPMQBE 199
DB 416 HAFQEBETGVRELAEEDDGEKIAIKLWIEDIKLK-----GKYKNE 460
QY 200 ALKVLVLLMDEGSALSRLKVLFPVQRLERRPPQASKTSIGHVOLLVYRASCFTKTRDE 259
DB 461 AIEP-----SFIDRDVPEVQVQEMVSGYVCEBDKTKAKIADR-- 501
QY 260 DGLMQLKEEPRSYEALRREHDAQIVHIAEAGLRISPQWSSLYGLDAHKSMMQSIID 319
DB 502 -VSLIKRREGR--QVREGECK-----KQESSLKQVEQSSASQGTGIX 544
QY 320 KIQSPBSFAKSVQELTYLQRTGDP-----ANLNRLRPHLELLANIDPNDVASPTW 371
DB 545 QLPASATGIPATSTTASVSTQVEEBEPADHQOLQVQOFAISVLS--DGTVDGQGS 602
QY 372 EQLENAMVAVKTVVGLVDFIQNYSRKGHET-----POPQNSKYTKSMCRDL 419
DB 603 VFTESKVSQQTVSIG-----SQHEQAHSTGVCHISTVQAQSQPHGYTPPSSVAG 656
QY 420 ROQGCPRGNTCTFASQBLEKYRLRNKNATVATPPLNKVGVNNTVTTAGNVISV 479
DB 657 QSQGQ-PSSSSLTGVSSSQPIQHPO-----QQQGIQGTAPQ----- 692
QY 480 IGSTETTKIVPSTNGISNAENSVSQILSRSDSTIRALETVKAKVKGAVGANGQNAQPSA 539
DB 693 -----QTVQYSLSQ-TSTSEBAT-----TAQPVSQPQA 719
QY 540 DGVTEKIKSPKTPVSNVATASAGSN--VGTELNSVPQKSPFLTRY-----PVPP 591
DB 720 PVLVP-QVSAQKQLPVSPVPTIQEPQIPVATQPSVVVHSGANFLPVGOPLPTILP- 777
QY 592 HSENIQFQDPRTOIIPFEVPOY--PQTGYPPPTVPAGVAPCVPRFVSNVPESSLP- 648
DB 778 -----QYVSQLPISITPHVSTAQTGFSLPITMAAGITQ--PLTLASSATTAIRQ 827
QY 649 -----PAMPYADHYSTSPDRMNSPY-----OPP-----PQYGPVPVPSGMYAV 694
DB 828 VSTVPSQLP-----TLQPTVQLPSQVHPQLQPAVSGMGPANLQGAAPVPLSSGDL 882
QY 695 YDSRRIMRPMYQORDIIRSNLPPMDVHSSVYQTSLEERYNSLDGYVAVACQPPSEPR 754
DB 883 YQGFPRRLPPQYPGSNNIAPSSNVASVCHISTYLAKPMPTEVLATPGVPTVQPVESN 942
QY 755 TTVPL-----PREPGHL-----KTSCEBOIRRRKPDQMAOYHTQKAPLVSTLPVATQ 802
DB 943 LVPVPGVGQVQVQVSGSLAQAPTTSSQAVLES-----TQGVQVAPAEVAVAA 994
QY 803 SP--TPSPPL-PSVDF-----RADFSESVSGTFEBEDHLSHYSPMCGTIGSCINAI 851
DB 995 QPQATOPTTLASSVDVAHSDVAGMDSGDNENVPSSSGRHEGRTTKRHYKSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNAVLMDLDSGDVKKRVHLEFETQRTKEEDPIIPSPGPIISKWG 906
DB 1055 TSRPKRLIINVSNGKGRVVECOLETHNRKMVTFFKFDLDGDNPEIATIMVNDPFI----- 1110

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QY 907 AISMSS-----RFGYHTTDPVOA-----TAQO---GSATKP 934
Db 1111 AIERSSFVDQVREIIEKADEMILSEDSVYEPBGDQGLESLQCKDDYFGSGQCKLEGEFFKQOP 1170
QY 935 ISVSDYVPYVNAVDSRMSYSGNEATSSAHYERPRFIYTDGSHRKSS---TEDDL-SL 990
Db 1171 IPASMPQOIGLPIPS-----SLTOVHVSAGR-RFIVSPVPSERLSKPIFSEIITDV 1222
QY 991 ELQOAKSNLSLLHOREANALAMQOKKWNLSDEGRHLTLNLSKEIIEJRNELQSDYTEDATD 1050
Db 1223 AASTAQSQSGMNLSHSASLSLQOAFS-----ELRRQW---TEGNT 1261
QY 1051 TKPDRD-----IELESLADTDEBDQSEPIEILD--IQLGISQNDQ 1092
Db 1262 APFNFHSHGTFFPVVPVPLSLIAGVPTAAATAPVPATSSPPNDISTSVIGSEVTVPTEE 1321
QY 1093 LLNGMAVENGHPVOOHOKEPPKQKQSLGEDHVLIEBKITLLPYTSCSQPLPVISINAS 1152
Db 1322 GIACVATSTGVVTSGLPIRP-----VSEEPVLSSVSSITPIPAVVISITTS 1368
QY 1153 -CLPITTSVS 1161
Db 1369 PSLQVPITSTS 1378

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RESULT 11
US-09-854-856-2
/ Sequence 2, Application US/09854856
/ Patent No. 6541252
/ GENERAL INFORMATION:
/ APPLICANT: Walke, D. Wade
/ APPLICANT: Hilbun, Erin
/ APPLICANT: Donoho, Gregory
/ APPLICANT: Turner, C. Alexander Jr.
/ TITLE OF INVENTION: No. 6541252e1 Human Kinases and Polynucleotides
/ TITLE OF INVENTION: Encoding the Same
/ FILE REFERENCE: LEX-0178-USA
/ CURRENT APPLICATION NUMBER: US/09/854, 856
/ CURRENT FILING DATE: 2001-05-14
/ PRIOR APPLICATION NUMBER: US 60/206,015
/ PRIOR FILING DATE: 2000-05-19
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 2382
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(2382)
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-2

Query Match          3.1%; Score 194; DB 2; Length 2382;
Beet Local Similarity 18.5%; Pred. No. 1.2e-05;
Matches 235; Conservative 167; Mismatches 70; Indels 362; Gaps 49;

QY      KACPFDDTAINT-----DIDVLPVNFFALLQVGAQVDPDHOSIKLSNIGEN 92
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      KRASFASVIGETPEFMAPMEWEYKIDSVDYVARGMCLLENATSEYP----- 421

QY      KHYEVAKKCVEDLALYLPKPLSGGKVASLNSAL-----SRPMQRKLVTLVN 139
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      ---YSEBCNAAQIYRRVTSVGR-PASFEDKVALPEVKEIIEGCIRONKBERYSIKOLN 475

QY      COLVEEGRGVAMPARASLIGERTVTEILIQHNPQOOLSANLMAVVRARCGFLPAMQEE 199
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      HAFQOEITGVAVELAEDEDDGSKIMIKMLRIEDIKKLK-----GKYDNE 520

QY      ALKVLVLALEDGSAISRVLYLVFVVOGLEPFPQASKTSIGHVQVLLYRASCFVYTKDE 259
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      AIEF-----SFLERIVDPDVAAQEWESGYVEGGHKTWAKAIKOR-- 561

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QY	260	DSLSMOLKEPBRSEALRREDDAQIVHIANEAGRISEPEOMSSILXYDLNKHMSMOISID	315
Db	562	-VSLIKRRERER--QIVREOEK--	604
QY	320	KLOSPESFAKVOELTIVLQRTGDP-----ANLRLRPHLELANIDPNPAVSPTW	371
Db	605	QLPBASTGCIPTASTTSSASVSTOVEPEEDADQHQLQYQOPSTIVLS--DOTVDSGOSS	662
QY	372	EOLENAMAVAKTVVHGLVDPIQYSRKGHEF-----PQOPNSKIKTSMCRDL	419
Db	663	VFTESRVSQOTVSYG-----SQHEQASHGTVPBGHIPSITVAQSOQPHGVPPSSVAOG	716
QY	420	RQOGCGRGTCFPAHSGOELEKXRLNKKNATVTRFPLLNKVCANNVTVTAGNIVSY	479
Db	717	QSOQO--PSSSLTGVSSOPIQHO-----QOQIGQOTAPQ-----	752
QY	480	IGSTETTGKIVPSTNGISMAENSVSOLISRSTDSLTALETFVKKGVKVGANGONAGPSA	539
Db	753	-----QTVQVSLSQ--TSTSSEAT-----TAQVSGPOA	779
QY	540	DSYVENKIGSPKTPPVNVAATSGAPSN--VGTILNSVPQKSSPFLTRY-----PYPP	591
Db	780	PQVLP--QVSAKQOLPVGQPVFTIGEBQIIPATOPSVVPHNGANFLPVGQPLTPLLP--	837
QY	592	HSENIQYFQDERTQIPEEPVQY--PQTGYVPPPTVAGVAPCVPRFRESNNVSSSLP--	648
Db	838	-----QYVSGIIPSTPHVSTAQIGFSSLPITMAAGITQ--PLTLIASSATTALIPG	887
QY	649	-----PASMYPADHYSTFSPDRMNSPY---QPP-----POPYGVPPVPYSGMTAVP	694
Db	888	VSTVVPSSLP-----TLQPVTOQLPQSVQVHQLLOPAVQSMGIPANLQOAAEVLPLSSGDVL	942
QY	695	YDSRRIRMPRYQORDDIIRNSLSPMDVMHSSVYQTSLRERYNSLDGYVSAVQCPSEPR	754
Db	943	YQGPPLRPLPOYPBDSNIAPESSNVA5CIHSTVLXPMPTFVULATPGYFPVVOYPBSN	1002
QY	755	TTVPL-----PREPCGHL-----KTSCEBQIRRKPDQMAQYHTOKAPLVSSTLPVATQ	802
Db	1003	LLVEMGVGQVQYQSGGSLAQAPRTSSQOAVLES-----TQGVSAQPAEPAVA	1054
QY	803	SP--TPPSPL-FSTVDF-----RADPSSVSQTRKEEDHLSHYFSWSCGTCGSCINAI	851
Db	1055	QPOATQPTTLASSVDASHDVASGMSGMBNVPSSGRRHGERTTKRHYKXSVNSRSRHEK	1114
QY	852	DSEKDYIAN-----SNAVIMDLDSGVCKERVHLEFQORTKEEDPIIPESDGP1ISKWG	906
Db	1115	TSRKALILAVNSKGDVVEBQLETHNRKAVTFPFDLGDNPEBIATIMVNNDFIL----	1170
QY	907	AISRS-----RTGHTTDPVOA-----TASQ--GSATKP	934
Db	1171	AIERSEFUDQVREIIEKADEMLSEDEVVEPEGDGLSLQKODYGFSGSQKLEGFEKOP	1230
QY	935	ISVGDYVPYNAVDSRKS5YGNEMT5SAHYVERPRLVITL5GHRKHS---TGDL--SL	990
Db	1231	IPASSMPOQIGIFTS-----SLTQVYHAGR-RFIVSPVPSRLRESKYFPELITDTV	1282
QY	991	ELQOAKSNNLLOREANALAMQCKMNSLDGBRHITLNL5KEI5LRNGELQSDTDEDATD	1050
Db	1283	AAS7AQBPCKMNL5HAS5SL5QCAF5-----ELRAQM---TEGPNT	1321
QY	1051	TKPRD-----IELE5ADTDPEPDQOSEPIEILD--TOLGISSONDQ	1092
Db	1322	APPF5HTGTPFVVPPL5SIAGVPTTAAATAPVATSSBPNDISTSV5QSEVTVTEE	1381
QY	1093	LLANMAVENGHPVQOHQKEPPKQKQSLGEDHVL5LEOKTILP5TSCFSQPLP5VINAS	1152
Db	1382	GIAVAVNSTGVN5SGLP5IP-----VSS5PLV5SVSSITIPAVV5ISTTS	1428
QY	1153	-CLPITTSVS	1161
Db	1429	PSLOVPTSTS	1438

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QY 649 -----PASMPRADHYSTFSPRDKNNSSPY-----QPP-----PQYGPVPPVPEBGMATVP 694
Db 888 VSTVPISQLP-----TLLOPVTOLPQSVHNPOLLQPAVQSGKIPANILQOAAEVLPISSGDVL 942
QY 695 YDSRRIRMPWYCRDDILIRNSLSPMKVMHSSVQTLREKXNSLDGYSAACOPSEPR 754
Db 943 YQGRPRPLPQYPCGDSNIAPESNVASVCHISTVLXPRMPEVIALTPGVPFTVQPVYESN 1002
QY 755 TTVPL-----PREPCGH-----KTSCEQIRKRDQMAQYHTQCAPLYSSLTPLVATO 802
Db 1003 LLVPMGGVGGOVQVSQPGSILAQAPTTSSQOAVLES-----TQGVSOVAPAPPAVA 1054
QY 803 SP--TPESPPL-FSYDF-----RADPSESVGTKFEEDHLSHYSPWSCGTTGSCINAI 851
Db 1055 QPQATQPTTLTASVDSASHDVAAGMSDGNBNVPSSGRHGGRTTKRHYKRSVRSRSHK 1144
QY 852 DSEKQVIAN-----SNAVLMDDSGVKRRVHLFEQRTKTEEDPIIPSDGFIISKWG 906
Db 1115 TSKRKLRLIWNKNGKRDVBCQLETHNRKRVTFKFDLDGDNPEIATIMVNNDFIL--- 1170
QY 907 AISRSS-----RTGYHTTDPVOA-----TASQ---GSATKP 934
Db 1171 AIEBESVVDQREIIEKADEMLSEDEVBEBOGGLSELGKODYGRSGSGKLEGEKQOP 1230
QY 935 ISVSDYPPYNAVANDSRMSSYGNENATSSAHYVERDRPIVTLDSGHRKSS---TGDLL-SL 990
Db 1231 IPASMSQOQIGIPTS-----SLTQVHHAGR-RFTVSPVPESRLESKVPSEIIDTV 1282
QY 991 ELQOAKSNSLLOREANALAMQCKWNSLDBGRHLLTMLSKIEELRANGELQSDYTEDATD 1050
Db 1283 AASTNAQPCMNULSHSASLSLQCAF-----ELRKAQM---TECPNT 1321
QY 1051 TKPRD-----LELELSADTDEPDDQSEPIEBILD--TQLGISSONDQ 1092
Db 1322 APPEFSHTGTPFPVPPFLSLIAGVPTTAATAATAPVATSSBPNDISTSVIQSEVTEPTEE 1381
QY 1093 LLNMAAVENGHPVQOQKPEPKOKKSLGEDHVLIEBOKTILPLVTSFCFQPLPVVISGNAS 1152
Db 1382 GIAGVAVTSTGVVTSGGPPIPP-----VSESPLSSVSVSSITIPAVVISITTS 1428
QY 1153 -CLEPITTSVS 1161
Db 1429 PSLQVPTSTS 1438

```

```

RESULT 12
US-10-010-720-2
; Sequence 2, Application us/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwen
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0382-USA
; CURRENT APPLICATION NUMBER: US/10/010,720
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; PRIOR FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2382
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2382)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-2

Query Match      3.1%; Score 194; DB 2; Length 2382;
Beet Local Similarity 18.5%; Pred. No. 1.2e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

48 KACPEDQTAINT-----DIDVLPVNFALLQVGAQVDPDHQSIKLSNIGEN 92
375 KRASFSAKSIIGTPEFAPMEYBEKYDESVDVYAFGCMLEMATSEVP----- 421
93 KRIEYAKKQVEDLALYLKPLSGGKGVASLNOSAL-----SRPMQKVLTVLN 139
422 -----YSECQNAAQIRRYTSGVK-PASFPKVAIPVKEIIBGCIKQNDERSISIDLIN 475
140 COLVEBEGRVAMRARSIGERTVELLIQHONPQOLSANMAAARQGFIPGMQBE 199
476 HAFPOETGVAVLEAEDDEKIAIKLWLRIDIKLK-----GKYKNE 520
200 ALKLVLLALEDGSAISRKVLVLFVVQRLPFRFQASKTSIGHVOLLYPASCFTYKRD 259
521 ALEF-----SEDLERDVPEVDVAQEMVESGYCEBDHHTMAKAIKDR--- 561
260 DSSLMOQKEEFPSYEALREHDAQIVHAMEAGLRISPQWSSLLGYDLAHKSHMOIID 319
562 -VSLIKRKEQR--QVREEQEK-----KQESLSLKQVEQSASQGTGIK 604
320 KQSPSPFAKSVQELTIVIQRTGP-----ANLRRLPHIELLANTDPNDASPTW 371
605 QLPASASTGIPATSTTSASVSTQVEEPPEADHQOQLOQOPSLISVLS--DGTVDSSQSS 662
372 EOLENAMVAVKTVVHGLVDFIQNSRKGHET-----PQOPNSKYTKSMCRDL 419
663 VTRESVSSQCIYSG-----SQHQASHTGIVPHGISVTVQAQSPHGIVPPSSVAG 716
420 RQGGCGPRTGCTFAHSGELEKYLRLNKKINATVTFPLLNKGVNNTVTTAGNVISV 479
717 QSGQCG-PSSSSLGVSSQPIQHPQ-----QQQGIQGTAPPO----- 752
480 IGTSTTGKIVPTNGISNAENSVQILSRSTDTSLALETVKKVKGANQGNAGPSA 539
753 -----QTVQVYLSQ-TSTSEAT-----TAQPVSOPOA 779

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540 DSVTENKIGSPKPTPVSNVAATSAGPSN--VETELNSVPQKSSPFLTRY-----PVYPP 591
780 PQVLP-QVSAGQQLVSPQVPFTIGEPQIPVATQSPVAVSHGAFHLPVGCPLPFLP 837
592 HSENIQTFQDRTQIPREVPQY--PQTGYPPRPVPAQVAPCFVRFRSNNVPSSSLP- 648
838 -----QYVSOQIPISTPHVSTAQTGFSSLPITMAGITQ--PLTLASSATTAALPG 887
649 -----PAMPVADHSTFSPDRMNSPY-----QPP-----POPYPVPVPSGVYAV 694
888 VSTVPSQLP-----TLQPTVQLPSQVHNPQLQAVQSMGIPALVQGALEVPSSGDL 942
695 YDSRRIMRPYQORDIIRNSLPRMDVHSSVQYTSLRERNYSLDGYVAVACQPPSEPR 754
943 YGCFPRRLPQYRGDSNIAPSNSVASCISHSTVLXPRMTEVLATPGYFPVYQYVESN 1002
755 TTVPL-----PREPGHL-----KTSCEBQIRRKPRDQMAQYHQAFLVSTLPVATQ 802
1003 LLVPMGVGGQYQVQSPGSLAQAPTTSSQAVLS-----TQVSGVAPAEVAV 1054
803 SP--TPPSPL-PSVDF-----RADFSESVGTKEEDHLSHPMSCGTIGSCINAI 851
1055 QPQATQPTTLASSVDSASDVASGMSDGENVPSSSGRHEGTTGRHYKKSVRSSRHEK 1114
852 DSEPRDVIAN-----SNAYLMDLSDGVKRVHLEFQRTYEEDPIIPSDGPIISKWG 906
1115 TSPFKLRILNVGNKGDVVECCLETHNRKMTVFKEFDLDGNDPEIATIMWNDFIL---- 1170
907 AISRSS-----RTGYHTTDPVQA-----TSQ-----GSATKP 934
1171 ATERSSFVDQVREIEIEKADMLSEBVSVERBEDQLESLOQKDDYGFSSQLEGEFKOP 1230
935 ISVSDVPYVNAVDSRWMSYGNEDATSSAHYVBRDFIYTDLSGHRKHS---TGDL--SL 990
1231 IASSMPQOIGIPTS-----SLTQVHSAQR-KFIVSPVESLUREKVPSEITDQV 1282
991 ELQAKSNLSLLQREANALAMQCKNSLDEGRHLLTNLSKEIELRNGSLQSDYEDATD 1050
1283 AASTAQSQPMNLISHASSLSLQAFS-----ELRRQM-----TEGPNT 1321
1051 TKPRPD-----IELESLDIDPEPDQOSEPIEILD--IQGISQONDO 1092
1322 ADPNFSHTGPTFPVVPPLISLAGVPTTAATAVPVPAITSSPNNDISTSYQSEVTPTE 1381
1093 LINGMAVENGVHVOHQKEPPKQKQSLGEDHVLVEBQKTLIPVTSQFQPLVPSISN 1152
1382 GIAGVATSGVVTSGGLPIPP-----VSESPVLSVSSITIPAVVISITTS 1428
1153 -CLPITTSVS 1161
1429 PSLQVPTSTS 1438

RESULT 13
US-09-854-856-48
; Sequence 48, Application us/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1939

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)....(1939)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-48

Query Match
Best Local Similarity 19.2%; Score 193.5; DB 2; Length 1939;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GKGVASLNQSLSPRMOKLVTLVNQCQVVEEGRVR-AMRAARSLGERTVELLIQHON 172
DB 660 GQSSSSSLTGVSSQPIQHPOQOQGIQQTAPPOQTQVSLSTSTSEKATTAQVPSQPA 719
QY 173 POOLSANLMAAVRANGCQFLGPA-----NOEALKLVLALDEGALSRRKVLVLFVQRL 227
DB 720 PQVLQVSAKQSTQGVSAVAPAVAVAQPOATQPTTLASSVDSAHSD---VASGMSDG 776
QY 228 ERFPOASTSTIGHVQVLLYRASCFKVTYKDEDSLMQK-----EEFRSTYALRRED 281
DB 777 NENVSSSGRHHGRTTKRYRKS-VSRSRHEKTSRPKRLINVSNNKGRVVECOLETHN 835
QY 282 AQIVHAMEAGRLSPQWSSILY-GDLAKHSMQSIIDKQSPESFAKSVQELTVLQR 340
DB 836 RKMVTFKFDLD-GDNEELATITVNNDFLIALERSEFVDQVREILKADMLSEDSVSP 894
QY 341 TGDPANLNLRPHLELLANID-----PNPDVSPTEQOLENAMAVALKT 384
DB 895 EGDQG-----LESLOGKDDYGFSGQKLEGFEKQPIFPASSMP--QQIGIPTSSLTQV 944
QY 385 VHGLVDFLQNYRKRKHETPQOPN-----SKYTSKCRDLRQCGCPRGCTNCTFAHS 436
DB 945 VH-----SAGRRFVSPVPSRLSESKVPSEIDTVAASTAQSPG-----NMLSHS 991
QY 437 QEELEKYR---LRNKI-----NATVTRTP---LNVGVNNTVTJTA--- 473
DB 992 ASSLSLQQAFFSELRRQMTGENTAPNFSHGPTFPVPPFLSLAGVPTTAAATAVP 1051
QY 474 -----GNVSVIGSTETGKIVPSTNGISNAENS-----VSQLS 508
DB 1052 ATSSPNDISTSVISQEV---VPTREAGIAGVATSGVTSGLPIPIPVSESPVLSVVS 1108
QY 509 RSTDTLRALETVKVKGKVGAN-----GQNAAGPSAD-SYENKIG---SPKPTPVSN 557
DB 1109 SITIPAVVSIITSPSLQVPTSTSEIVASTALYPSVTASATASAGSGTATPGKPAV 1168
QY 558 VAATGAGPSNVGTETNSV-----PQSSPFLTRVPVYPHSENIOXF 599
DB 1169 VSQQAAGSTTVGATLTSVTTTSPSTASQLSIQSSSTSTPTLAEVVVAASHLD-KTS 1227
QY 600 QDPRTQIPREVPQYQOTGYRPPPP-----TVPAGVAPCV-PRFVSNNNPESLSPPASMP 653
DB 1228 HSTTGLANSL-SAPSSSSSPGAGVSYISQPGHLPLVIPSIVASTPLLPQAAGTSTFP 1286
QY 654 YADHSTSEPRDRMSSPYQPPPPQYGVPPVPSGM-----YAPVDS 697
DB 1287 L-----LPQVPSIPLVQPVANVPVQQTLLHSQPOPALLPMPHPTHCPEVDS 1334
QY 698 RRIWRPMWQRODDI-----IRS--NSLPRMDVMHSSV-YQTSLRERNVSLDGYVSA-- 746
DB 1335 DT--QPKAPGIDIDITLKEKLSLFESEHSSGAQHAASVLETSVLESTVTGPIPTTAA 1392
QY 747 -----CQPSSE-PRITVPLPREPC---GHILKTSCEEQIIR-KPDQMAQYHTOKA 790
DB 1393 PEKLLTSTTSLGPTNLPLGLTALPVTVTPGVQSTVSTTSSVKRGCT---APSKP 1448
QY 791 PLVVS- TLPVATQSPPTPSPPLFSVDFRADFSSESVSSTKFEEDHLSHYSPWSCGTIGSCIN 849
DB 1449 PLTKRPAVLPVGTGLP-----AGTLPS--E 1470
QY 850 AIDSEPKDVITANSNVIMDLDS-----GDVYRVRVHLFETQRRTK----- 888
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DB 1471 QLPFRPGESLITQSPLELDDQLRRTLSPEXITVTSANGVSPMAAPTAITEAGTQPOKG 1530
QY 889 ----BEDPIIPSPDPIISKWG-----AISRSSRTGYHTTDPVATASQSAATKPIVS 938
DB 1531 VSQVKEGPVLTATSGAGVFKWGRPQVSVAAQDAQKEGKKKSBDKASVHFESTSESSVLS 1590
QY 939 DYVPYVNAV-----DSRMSYGNENAT-SAHYVERDRFIYTDLS---G 977
DB 1591 SSSPSTLTKPRPNIGITIPGSSDVPESAHKTTASBEAKSDTQPTKVGFRFOVTTANKVG 1650
QY 978 HRKHSSTGDLSS-----LELQQAQNSNLLQREANALAMQKMN----- 1016
DB 1651 RFSVSKTEKIDTDTKKEGVASPPRMDLEQAVLPVPIPKERPELSEPHLNGPSSDPPA 1710
QY 1017 ----SLDEGR--HITNLISKEIELRN-----GELQSDY-TEDATDTKPRDRIEL 1061
DB 1711 AFLSRDVEDDSSGSPHPSQSLSPQVLSQSLSNSFNSSYSMSDNESEDIEDIKLEL 1770
QY 1062 SALDDEPDPQSEPIEILIDQLGISSONDQLN-----GMAVENGHVPVOHQKEPRK 1114
DB 1771 RRL-----RDKHLKEIQDLSRQKHETLSLYTKGKVPVAVIIPPAAPLGGRRRPTK 1823
QY 1115 OK-----KQSLGEDH-----VILEQKTLIPVTSQFSGQPLVPSISNACLP 1155
DB 1824 SKGSKSSRSSSLGKNSPOLSGNLSCQSAASVLIHPQOTLHPGN-----IPESGQNLQOP 1878
QY 1156 ITTSVSAGNL 1165
DB 1879 LKPSPSDDL 1888
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RESULT 14
US-10-010-720-48
; Sequence 48, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwen
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/010,720
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 48
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)....(1939)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-48
```

```

Query Match
Best Local Similarity 19.2%; Score 193.5; DB 2; Length 1939;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GKGVASLNQSLSPRMOKLVTLVNQCQVVEEGRVR-AMRAARSLGERTVELLIQHON 172
DB 660 GQSSSSSLTGVSSQPIQHPOQOQGIQQTAPPOQTQVSLSTSTSEKATTAQVPSQPA 719
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QY 173 POOLSANLMAVRAGCQFLGPA-----MOEALKVLVLLALDGSALSKVLVLFVQRL 227
Db 720 POVLPOVSAGKOSTGVSGVAPAEPAVAQAPOATPPTLIASSVDSAHSD---VASGMSDG 776
QY 228 EPRFQASKTSIGHVVOULLYRASCFKVTKRDESSIMQK-----EPRSYEALREHD 281
Db 777 NENVSSSGRHEGRTTKRHRYKS--VRSRREKTSRPKLRILNVSNGKGRVVECOLETHN 835
QY 282 AOIYHAMEAGLRISPEQMSLLY--GDLAHKSMMOSIIDKLOSPESFAKSVQELTIVLOR 340
Db 836 RKMVTFKFDLD--GDNPEBIATIMVNNDFILALERSFVDQVREIIEKADMEMLSEDEVSRP 894
QY 341 TGDPANLRLRPHLELANID-----PNPDVSPTEQOLENAMAIVKTV 384
Db 895 EGDQO-----LSLQCKDDYGFSGSKLEGEFKQPIIPASSMP--QOIGIPTSSLTQY 944
QY 385 VHGLVDFIOWYARKHETPOPOP-----SKYKTSKCRDLROQCGCPRGNTCTFAHS 436
Db 945 VH-----SAGRRFIVSVPRSLRESKVPFSEITDVAASTAQSPG-----NMLSHS 991
QY 437 OELEKYR---LRNKI-----NATVRTPP-----LNLKVGNNTVTTTA--- 473
Db 992 ASLSLQAFSELRAQMTGEPNTAPNFSHTGPTFPVVPPLSLIAGVPTTAATAVP 1051
QY 474 -----GNVIVIGSTETGKIVPSTNGISNAENS-----VSOLIS 508
Db 1052 ATSSPNDISTVIOSEVT---VPTBEGIAGVATISGVVTSGLPIIPYSESPVLSSVVS 1108
QY 509 RSTDSTLRALETVKVKGXGAN-----GQNAAGPAD--SVTENKIG---SPKTPVSN 557
Db 1109 SITIPAVVASISTSPSLQVPTSTSEIVASTALYPSVTSASAGSSTATPGKXPAY 1168
QY 558 VAATAGBNNGTELSV-----POKSSPFLRVPIYPHSHENIQCF 599
Db 1169 VSQAGASTTGATLTSTSTTSFBSTASQLSIQSSSTSTPLLETVVASAHSD--KTS 1227
QY 600 QDPFQIPEVPOYQOTGYPPPP-----TPVAGVAPCV--PRFVSNPNPESSLPPASMP 653
Db 1228 HSTTGIAFSL--SABSSSSSPAGVSYISQGLHPLVIPSIVASTPLLPQAGTSTFP 1286
QY 654 YADHYSTFSPDRMNSPPYOPPPPOPYGVPVPSGM-----YAEVDS 697
Db 1287 L-----LPQVPSIPLVQPVANVPAVOQLIHSPQOPALLPQPHTHCEVDS 1334
QY 698 RRIWPMYQORDI-----IRS--NSLPRMDVMHSSV--YQSLARKVNSLQGYVA-- 746
Db 1335 DT--QPKADGIDIKTLEKLSLSESHSSGAQHASVLETSVLESTVTPRPIPTTAVA 1392
QY 747 -----CQPSSE--PRTTVPLPREPC--GHUKTSCBEOIRK--KPDQMAQVHTOKA 790
Db 1393 PSKLLSTSTSLCPRTNPLGLTVALPVTVPVTPGQVSTVSTTSQVKGDT---APSKP 1448
QY 791 PLVSS--TLPVATQSPTPSPPLFSVDFRADPSESVSSTKFEEDHLSHYSPWSCCTIGSCIN 849
Db 1449 PLTKAPVLVGTGLP-----AGTLPS--E 1470
QY 850 ALDSEKQVIANSNAMLMDS-----GDVYKRVHLEFQORRK----- 888
Db 1471 QLPPEFGPSLTOSQOPLDLDLQALRRTLSPEKITYTSAVGPVSMAPTAITTEGTPQOKG 1530
QY 889 -----EEDPIIFSDGPIISKWG-----AISRSSRTGYHTDPVQATASQATKPISVS 938
Db 1531 VSQVKEGPIVLAISGAGVFKMGRFQVSVADAGAKQKSKSEDAKSVHFESSSTSESVLS 1590
QY 939 DVVPYVNAV-----DSRWSSYGNBATS--SAHYERDRPIYTDLS--G 977
Db 1591 SSSPESTLVKPEPNGITIPGISDVPESAHKTTASBAKSDTQPTKYGFOVYTTANKVG 1650
QY 978 HKHKSSTGLLS-----LELOAKSNSLLQREANALAMQOKM----- 1016
Db 1651 RFSVSTTEKTIIDTKKEGPVAPSPFMDLQAVLPAVTPKKEKELSEPSHLNPSDDPRA 1710
QY 1017 -----SLDEGR--HLLNLNLSKEILRN-----GELQSDY--TEDATDTKPPDRIDLEL 1061

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Db 1711 AFLSRDVEDDGGSGSPHSRPHQLSKSLPSQNTLBOSLSNFSNWSMDNSDIEDDLKLEL 1770
QY 1062 SALDTDEPDGQSEPIEELIDTQLGISQNDOLN-----GMAVENGHPVQOHOKEPPK 1114
Db 1771 RRL-----RDKHKEIIDLQSRQKHEIESLYTKGVPPAVIIPAPISGRRRRPTK 1823
QY 1115 OK-----KOSIGEDH-----VILEQKTLIPVTSFCSPQLPVISNASCIP 1155
Db 1824 SKGSKSSSSSSSLGKNSPOLSGNLGSGASAASVHLPOQTILHPON-----IPESGQNLQOP 1878
QY 1156 ITTSVSAQNL 1165
Db 1879 LKPSPSDNL 1888

RESULT 15
US-09-854-856-16
; Sequence 16, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hildun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854, 856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1999
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1999)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-16

Query Match 3.1%; Score 193.5; DB 2; Length 1999;
Best Local Similarity 19.2%; Pred. No. 8.5e-06;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GKGVASLMSQALSRRMORKVTLVNCQIVBEGRYR--AMRAARSIGERTVTELLIQON 172
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QY 173 POOLSANLMAVRAGCQFLGPA-----MOEALKVLVLLALDGSALSKVLVLFVQRL 227
Db 780 POVLPOVSAGKOSTGVSGVAPAEPAVAQAPOATPPTLIASSVDSAHSD---VASGMSDG 836
QY 228 EPRFQASKTSIGHVVOULLYRASCFKVTKRDESSIMQK-----EPRSYEALREHD 281
Db 836 RKMVTFKFDLD--GDNPEBIATIMVNNDFILALERSFVDQVREIIEKADMEMLSEDEVSRP 894
QY 282 AOIYHAMEAGLRISPEQMSLLY--GDLAHKSMMOSIIDKLOSPESFAKSVQELTIVLOR 340
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QY 341 TGDPANLRLRPHLELANID-----PNPDVSPTEQOLENAMAIVKTV 384
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QY 385 VHGLVDFIOWYARKHETPOPOP-----SKYKTSKCRDLROQCGCPRGNTCTFAHS 436
Db 1005 VH-----SAGRRFIVSVPRSLRESKVPFSEITDVAASTAQSPG-----NMLSHS 1051
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Job time : 37 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:51:25 ; Search time 112 Seconds
(without alignments)
4925.794 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215
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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6215	100.0	1191	5	US-10-619-992-2 Sequence 2, Appl1
3	6207	99.9	1191	3	US-09-921-099-4 Sequence 4, Appl1
4	6207	99.9	1191	5	US-10-619-992-4 Sequence 4, Appl1
5	5483	88.2	1048	5	US-10-485-225-8 Sequence 8, Appl1
6	1538	24.7	819	6	US-11-097-143-24915 Sequence 24915, A
7	843	13.6	1048	5	US-10-619-992-11 Sequence 11, Appl1
8	611	9.8	522	4	US-10-104-047-3665 Sequence 3665, Ap
9	611	9.8	522	6	US-11-072-512-3665 Sequence 3665, Ap
10	490	7.9	95	3	US-09-867-550-1346 Sequence 1346, Ap
11	311	5.0	67	3	US-09-864-761-48290 Sequence 48290, A
12	267	4.3	276	5	US-10-450-763-41493 Sequence 41493, A
13	208	3.3	1552	5	US-10-330-773-941 Sequence 941, App
14	207	3.3	2377	6	US-10-840-512-196 Sequence 196, App
15	203	3.3	674	6	US-11-096-568A-27755 Sequence 27755, A
16	203	3.3	786	6	US-11-096-568A-27755 Sequence 27755, A
17	203	3.3	1267	4	US-10-092-900A-128 Sequence 128, App
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24	195	3.1	2135	4	US-10-362-892-9 Sequence 9, Appl1
25	195	3.1	2382	4	US-10-196-935A-2 Sequence 2, Appl1
26	195	3.1	2382	4	US-10-052-648A-40 Sequence 40, Appl
27	195	3.1	2382	4	US-10-336-472-230 Sequence 230, App

28	195	3.1	2382	4	US-10-408-765A-1404 Sequence 1404, Ap
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30	194.5	3.1	1579	5	US-10-330-773-939 Sequence 939, App
31	193	3.1	2108	5	US-10-491-467-2 Sequence 2, Appl1
32	192.5	3.1	1390	4	US-10-092-900A-224 Sequence 224, App
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35	191.5	3.1	2816	5	US-10-291-128-145 Sequence 145, App
36	191	3.1	1129	5	US-10-840-512-119 Sequence 119, App
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40	190	3.1	922	4	US-10-437-963-125036 Sequence 125036, A
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44	185.5	3.0	2325	4	US-10-663-433-2 Sequence 2, Appl1
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ALIGNMENTS

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RESULT 1
US-09-921-099-2
; Sequence 2, Application US/09921099
; Patent No. US20020107372A1
; GENERAL INFORMATION:
; APPLICANT: Hefenider, Steven
; APPLICANT: Merkins, Robert
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921,099
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      181 WAAVARGGQFGLPMQOEALKVLVLALEDGSAISKVLFVVOQLERFPQASTSIG 240
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DB      181 WAAVARGGQFGLPMQOEALKVLVLALEDGSAISKVLFVVOQLERFPQASTSIG 240
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DB      301 SGLLYGDLAKHSMOSIIDKLOSPESFAKSVDELITVLOTGDPANLNLRLPLELLANI 360
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RESULT 2
US-10-619-992-2

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; Sequence 2, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
; LENGTH: 1191
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-619-992-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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; Sequence 4, Application US/09921099
; Patent No. US2002010732A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkin, Steven
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-921-099-4

Query Match 99.9%; Score 6207; DB 3; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAVOAQAQWTEFLSCPTCYNEFDENHAKPISLGCSTVCTCLNKLHKKACPFQDTAIND 60
QY 61 IDVLVFNFLDLGVAGQVDHOSIKLSNGENKHYEVAKKVEEDLALYLKPLSGGKGVAS 120
DB 61 IDVLVFNFLDLGVAGQVDHOSIKLSNGENKHYEVAKKVEEDLALYLKPLSGGKGVAS 120
QY 121 LNSALSRPMQKRLVTLVNCQVEEGRVYRAMPAAASLGERVTTELLOHONPOQLSANL 180
DB 121 LNSALSRPMQKRLVTLVNCQVEEGRVYRAMPAAASLGERVTTELLOHONPOQLSANL 180
QY 181 WAAVBARCGQFLGPAWQEBALKVLIALFDGSLSKVLVLFVQRLERFPQASTSIG 240
DB 181 WAAVBARCGQFLGPAWQEBALKVLIALFDGSLSKVLVLFVQRLERFPQASTSIG 240
QY 241 HVOVLVYRASCFKMTKRDSDSSLMOLKEFRSYEARRRHDDQIVHIAEAGRISPEQM 300
DB 241 HVOVLVYRASCFKMTKRDSDSSLMOLKEFRSYEARRRHDDQIVHIAEAGRISPEQM 300
QY 301 SSLVYGLDLAKHSMOSIIDKLOSPEFAKVOELITVLQRTGDPANLRLPHLELLANI 360
DB 301 SSLVYGLDLAKHSMOSIIDKLOSPEFAKVOELITVLQRTGDPANLRLPHLELLANI 360
QY 361 DNPDPAVSTTWQOLENAMAAYKTVVHGLVDFTONYSRKKEHPPOPPNSKYKTSKRDLR 420
DB 361 DNPDPAVSTTWQOLENAMAAYKTVVHGLVDFTONYSRKKEHPPOPPNSKYKTSKRDLR 420
QY 421 QGGGCRGNTCTFAHQSELEKYLANKKINATVTFPLINKGVNNTVTTAGNVISYI 480
DB 421 QGGGCRGNTCTFAHQSELEKYLANKKINATVTFPLINKGVNNTVTTAGNVISYI 480

DB 421 QGGGCRGNTCTFAHQSELEKYLANKKINATVTFPLINKGVNNTVTTAGNVISYI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTSTLPALETYKVGKVGANGQNAAGPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTSTLPALETYKVGKVGANGQNAAGPSAD 540
QY 541 SYTENKIGSPKTPVSNVAATISAGSNVGTELSVPQKSPFLTRPVYPPHSENIQYQC 600
DB 541 SYTENKIGSPKTPVSNVAATISAGSNVGTELSVPQKSPFLTRPVYPPHSENIQYQC 600
QY 601 DPTQIPEFVPOYPTQYVPPPTVAGVAPCVPRFVRSNNVPESLPASMPYADHYST 660
DB 601 DPTQIPEFVPOYPTQYVPPPTVAGVAPCVPRFVRSNNVPESLPASMPYADHYST 660
QY 661 FSPDRMNSPYQPPPOYGVPPVPSGMVAPVYDSRIIMRPMTQORDIIRSNLPPM 720
DB 661 FSPDRMNSPYQPPPOYGVPPVPSGMVAPVYDSRIIMRPMTQORDIIRSNLPPM 720
QY 721 DVMHSSVYQTSIREYVNSLDGYVVAACOPSPSPRTTVPLEPRPCGHLKTSCEBQIRKPD 780
DB 721 DVMHSSVYQTSIREYVNSLDGYVVAACOPSPSPRTTVPLEPRPCGHLKTSCEBQIRKPD 780
QY 781 QMAQYHTOKAPVYSSSTLPVATOSPPTPSPPLFSDVDFRADSESVSQTKFEEDHLSHSPMS 840
DB 781 QMAQYHTOKAPVYSSSTLPVATOSPPTPSPPLFSDVDFRADSESVSQTKFEEDHLSHSPMS 840
QY 841 CGTIGSCINADISEPKDVIANNAVIMDIDSGDVKRHYLFFETORTKEEDPIIPSDGP 900
DB 841 CGTIGSCINADISEPKDVIANNAVIMDIDSGDVKRHYLFFETORTKEEDPIIPSDGP 900
QY 901 IISKMGATSRSSRTGYHTTDPVQATASQGSATKPISSVSVYVYVYVAVDWRMSYGEATS 960
DB 901 IISKMGATSRSSRTGYHTTDPVQATASQGSATKPISSVSVYVYVYVAVDWRMSYGEATS 960
QY 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
DB 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
QY 1021 GHLLTLNLISKEIEIRNGELQSDYTEDATDTPKDRDIELELSALDDEDDGSEPIEEL 1080
DB 1021 GHLLTLNLISKEIEIRNGELQSDYTEDATDTPKDRDIELELSALDDEDDGSEPIEEL 1080
QY 1081 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKKSLGEDHVLIEBQKTLIPVTSCE 1140
DB 1081 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKKSLGEDHVLIEBQKTLIPVTSCE 1140
QY 1141 SQPLPVSISNASCLPITTSVSAGNLLIKTHVSEDKNDLKEVANGKMNVS 1191
DB 1141 SQPLPVSISNASCLPITTSVSAGNLLIKTHVSEDKNDLKEVANGKMNVS 1191

RESULT 4
US-10-619-992-4
; Sequence 4, Application US/10619992
; Publication No. US2005023163A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkin, Steven
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619, 992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921, 099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-619-992-4

Query Match 99.9%; Score 6207; DB 5; Length 1191;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MPVQAQWTEFLSCPICYNEFDENVHAKPISLGCSTHVCCTCKLHKRKAQCPFDQTAINTD 60
DB 1 MAVQAQWTEFLSCPICYNEFDENVHAKPISLGCSTHVCCTCKLHKRKAQCPFDQTAINTD 60
QY 61 IDVLVFNFFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
DB 61 IDVLVFNFFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
QY 121 LMQSALSRMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELLQHNQPOOLSANTL 180
DB 121 LMQSALSRMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELLQHNQPOOLSANTL 180
QY 181 MAABARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVQRLBFRPQASKTISIG 240
DB 181 MAABARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVQRLBFRPQASKTISIG 240
QY 241 HVVOLLYRASCFKVTYKRDSSLMQKEFRSYEARREHDAQIYHIAEAGLRISPEQW 300
DB 241 HVVOLLYRASCFKVTYKRDSSLMQKEFRSYEARREHDAQIYHIAEAGLRISPEQW 300
QY 301 SSLVGDGLAHKSHMOSIIDKLOSPESFAKSVQELTVLQRTGDPANLNLRLPHELLANI 360
DB 301 SSLVGDGLAHKSHMOSIIDKLOSPESFAKSVQELTVLQRTGDPANLNLRLPHELLANI 360
QY 361 DPNPDVSPTEWQLENAWAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSMCRDLR 420
DB 361 DPNPDVSPTEWQLENAWAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSMCRDLR 420
QY 421 OQGGCGRGNTCTPFAHQEBLEKYLRLNKKINATVTRFFPLNKYGVNNYTTTAAGNVSYI 480
DB 421 OQGGCGRGNTCTPFAHQEBLEKYLRLNKKINATVTRFFPLNKYGVNNYTTTAAGNVSYI 480
QY 481 GSTETTGKIVPSTNGISNAENSVQSLISRTDSTLRALETVKVKGKVGANGONAAQPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVQSLISRTDSTLRALETVKVKGKVGANGONAAQPSAD 540
QY 541 SVTENKISPPKTPVSNVAATSGPNSVGTSLNSVPOKSPFLTRVPVYPHSENIQYRQ 600
DB 541 SVTENKISPPKTPVSNVAATSGPNSVGTSLNSVPOKSPFLTRVPVYPHSENIQYRQ 600
QY 601 DRTQIPFEVPOYPOTGYRPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
DB 601 DRTQIPFEVPOYPOTGYRPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
QY 661 FSPRDMNNSPYOPPPQYGPVPPVPSGMVYAVVYDSRRIWPPMYQORDIIRKNSLPPM 720
DB 661 FSPRDMNNSPYOPPPQYGPVPPVPSGMVYAVVYDSRRIWPPMYQORDIIRKNSLPPM 720
QY 721 DVWHSVYQTSLRERYSNLDGYYSVACQPPSEBRTTVPLPREBCGLKTKSCBQIRKPD 780
DB 721 DVWHSVYQTSLRERYSNLDGYYSVACQPPSEBRTTVPLPREBCGLKTKSCBQIRKPD 780
QY 781 QMAQYHTQAPLVSSSTLPVATOSPTPSPSLFSDPRADPSESISGCKFEEDHLSHSPMS 840
DB 781 QMAQYHTQAPLVSSSTLPVATOSPTPSPSLFSDPRADPSESISGCKFEEDHLSHSPMS 840
QY 841 CGTIGSCINAIIDBRPDVIANSNVAMLDSDGKVRVHLFETQRTKEEDPIIPPSDGP 900
DB 841 CGTIGSCINAIIDBRPDVIANSNVAMLDSDGKVRVHLFETQRTKEEDPIIPPSDGP 900
QY 901 IISKWCAISRSRSTGYHTTDPVOATASQGSATKPIISVDVYPVNAVDSRWSSYGEATS 960
DB 901 IISKWCAISRSRSTGYHTTDPVOATASQGSATKPIISVDVYPVNAVDSRWSSYGEATS 960
QY 961 SAHYVERDRFIVTDLSGHRKHSSTGDLSTLEQAAKSNLILQREANALAMQKMSLDB 1020
DB 961 SAHYVERDRFIVTDLSGHRKHSSTGDLSTLEQAAKSNLILQREANALAMQKMSLDB 1020

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QY 1021 GRHLTLNLISKEIEBRLNGELSDYTEDATDTYKPRDRIDIELLSALDTPDEPGOSEPIEIL 1080
DB 1021 GRHLTLNLISKEIEBRLNGELSDYTEDATDTYKPRDRIDIELLSALDTPDEPGOSEPIEIL 1080
QY 1081 DIQIGISSQNDOLINGMAVENGHPIVQHQKEPPKXQKQSGSDHYVILEBQKTIILPTSCF 1140
DB 1081 DIQIGISSQNDOLINGMAVENGHPIVQHQKEPPKXQKQSGSDHYVILEBQKTIILPTSCF 1140
QY 1141 SGPLEVISISNASCLEPITTSVSAGNLIILKTHVMSDEKNDPLKFPVANGKWN 1191
DB 1141 SGPLEVISISNASCLEPITTSVSAGNLIILKTHVMSDEKNDPLKFPVANGKWN 1191

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RESULT 5

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US-10--485-225-8
; Sequence 8, Application US/10485225
; Publication No. US20050181355A1
; GENERAL INFORMATION:
; APPLICANT: Greener, Tavika
; APPLICANT: Moskowitz, Haim
; APPLICANT: Reiss, Yuval
; APPLICANT: Alroy, Iris
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE OF INVENTION: MODULATION OF VIRAL MATURATION
; FILE REFERENCE: PRL-P02-001
; CURRENT APPLICATION NUMBER: US/10/485,225
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/345,846
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-225-8

```

Query Match 88.2%; Score 5483; DB 5; Length 1048;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPVQAQWTEFLSCPICYNEFDENVHAKPISLGCSTHVCCTCKLHKRKAQCPFDQTAINTD 60
DB 1 MPVQAQWTEFLSCPICYNEFDENVHAKPISLGCSTHVCCTCKLHKRKAQCPFDQTAINTD 60
QY 61 IDVLVFNFFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
DB 61 IDVLVFNFFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
QY 121 LMQSALSRMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELLQHNQPOOLSANTL 180
DB 121 LMQSALSRMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELLQHNQPOOLSANTL 180
QY 181 MAABARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVQRLBFRPQASKTISIG 240
DB 181 MAABARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVQRLBFRPQASKTISIG 240
QY 241 HVVOLLYRASCFKVTYKRDSSLMQKEFRSYEARREHDAQIYHIAEAGLRISPEQW 300
DB 241 HVVOLLYRASCFKVTYKRDSSLMQKEFRSYEARREHDAQIYHIAEAGLRISPEQW 300
QY 301 SSLVGDGLAHKSHMOSIIDKLOSPESFAKSVQELTVLQRTGDPANLNLRLPHELLANI 360
DB 301 SSLVGDGLAHKSHMOSIIDKLOSPESFAKSVQELTVLQRTGDPANLNLRLPHELLANI 360
QY 361 DPNPDVSPTEWQLENAWAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSMCRDLR 420
DB 361 DPNPDVSPTEWQLENAWAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSMCRDLR 420
QY 421 OQGGCGRGNTCTPFAHQEBLEKYLRLNKKINATVTRFFPLNKYGVNNYTTTAAGNVSYI 480
DB 421 OQGGCGRGNTCTPFAHQEBLEKYLRLNKKINATVTRFFPLNKYGVNNYTTTAAGNVSYI 480

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Db 721 ASTFDPVTGSSMLSIY-----GPLICPK-----SSTTG 747

RESULT 7
US-10-619-992-11
; Sequence 11, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Heleneider, Steven
; APPLICANT: Mettner, Robert
; APPLICANT: Bennett, Robert
; APPLICANT: Seiser, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619, 992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent version 3.0
; SEQ ID NO 11
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-619-992-11

Query Match 13.6%; Score 843; DB 5; Length 1048;
Best Local Similarity 30.6%; Pred. No. 5,4e-49;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

4 QAAOWTEFLSCPICYNEFDENVHAKPISLCSHTVCKTCKINKLHR--KACPFDTAINTDI 61
Db 6 QGGQHQEVLCSICNHFNE-TFLPVSILCGHYICKAKREKNOYKPCPHDMKTTTSP 64
QY 62 DVLPNVFNALLDVGAVPRHOSIKLSNLSGKNRYEAKKCEDELLYLKPLSGKGVASL 121
Db 65 SEYPPNVALLSVY---FPRKQCTWLSGAVSEAKRVDLSIQ-IAKFFREADSERG-GTV 119
QY 122 NOSALSRPMQRLVTLVNCQULVEEGRVAVMRAARSLGERTVELLHONPOQLSANIM 181
Db 120 SREISRTLOKRYLALCYQREVDGRKLTKMKCRISERWMEILISQSNTHVSQIM 179
QY 182 AAVRARGCOFLPAMOEALKVLALLEDGALSRLVLFVVOLEPRFPQASKTISGH 241
Db 180 SAVRARGCOFLPAMODVLRILMLTLEGECLARKLVVYVQTLASDYPQVSKTCVGH 239
QY 242 VVQLTRACCFKTKRDESSLMQLEPRSYALRREDAQVHIAAMEAGLRISFEQMS 301
Db 240 VVQLTRACCFVNLKRDGSSLMQLEPRSYALRREDAQVHIAAMEAGLRISFEQMS 299
QY 302 SILYGLAKSHHQSIIDKLQSPESPAKSVQELTIVLQRTGDPAN-----LNRLRP 352
Db 300 ALLYADQSHRSHQSIIDKLQSPESPAKSVQELTIVLQRTGDPAN-----LNRLRP 356
QY 353 HUELLANIDPNDAVSPTEOLENANAVAVTVVHGLVDFIIONY---SRKHETPQOPNS 409
Db 357 CLEFFAGIEHEDTSMGMIDALHQIRILK--LHCGQDLRKMPKEERGVIILQARVPGG 414
QY 410 KYTSMCRDLRQGGCPRGTCNCTFAHSELEKRYLRANKKINATVATPFLNKVGNNTV 469
Db 415 -----MGGGPGGSG-----GAEGRI----- 430
QY 470 TTTAGNVISIGSTETTKIIVPSTNGISNAENSVSLISNSTDTSLRALETVKGVGVA 529
Db 431 -----GGLHPYISQIDETGKISRTNPKDSSANSPO----- 461
QY 530 NGQNAAGPSADVTEKNGISPPKTPVSNVAATSAAGSNVGTSLNSVPOKSSPFLTRVPY 589
Db 462 -----TPKQPRQKRYQWGIPIPNRMG-----YSSDAPEPIPSHQOQ 497
QY 590 PPHSENIOYFQDPRTOIPFEVPOYPOTGYPPPPPTVPAGVAPVPPFVSNVNPBESSLP 649
Db 498 PPP-----OFFNS--OHLPRFRGQRQAGAPPPPPPP-----MPLIGYD-----MPG 539

Db 721 ASTFDPVTGSSMLSIY-----GPLICPK-----SSTTG 747

RESULT 8
US-10-104-047-3665
; Sequence 3665, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3665
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match 9.8%; Score 611; DB 4; Length 522;
Best Local Similarity 34.1%; Pred. No. 2,3e-33;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

618 YTPPPTVAGVAPCYPRFRVSNVPESSLPASMWYADHYTFSPDRDMNSPYPPPP 677
Db 2 YTPPPTVAGVAPCYPRFRVSNVPESSLPASMWYADHYTFSPDRDMNSPYPPPP 677
QY 678 QYGPVPPVPSGVAPVYDSRRIMRPMYQDDILRSNLSLPPMDVHSSV--YOTSLSR 735
Db 50 Q-----YPPY-----YPSHYGRVYPAFSTREIFPESPI-PIEIPPAVPSVPSRR 100
QY 736 YNSLDGYVSACQ-----DS-----EPRTVPLPREFCGLKTSCEQIRKPDQWQYHT 787
Db 101 YQIESGYVVAHPHQIRPSYLRPEYSRLPPPPPP-----HSLDELHRRRKEIMQLBE 156
QY 788 QKAPLVSTLPVATQSPPTPSPPLFSVDFRADSESYSGTKEFEDHLSHPMSCGTIGSC 847
Db 157 RK--VISPPPPA-PSPTLP-PTFHEEFLBEDLKVAG-KYKANDYSQISPMSCDTIGST 210
QY 848 INAIDSEPDVIANNAVLMDLSDGVKRRVHLFETORRTKE--EDPIIPFSDGPIISKW 905
Db 211 IGTGKAKPKDVVAAGSVEMANNYSKGM--RDQRLDQRAAETSDDDLIPGDRPTVSRF 268
QY 906 GAISRSRTGYHTTDFVQATASOGATKPISVSDIYFYVNAVDSR--SSYG--NEATSS 961
Db 269 GAISRTSKTIYQAGQPMQAPQCAPTKSINISDVPY--GTHGCGASPYSPHONI 936
QY 962 AHYVERDRPIVNDLSHRK--HSTGDLSTLEQO-----AKSNSILLOR 1004
Db 327 GHFSERERISMSVASHGRPLPSAREQRLLEQOHNQISQOTQLRGPAVSNRLVLOK 386
QY 1005 EANAALMQO-----KNNSLDEGRHLTLANT--LSKEIELNNGELQSDYTEDATDKPD 1054
Db 387 EANTLAGQOPPPPPPKPMGMSQQLDELHQVRELGKTRRELISM--NQSLSLMK-- 443
QY 1055 RLIELESLALDDE--PDQSEPIEILDIQUGISSQNDQLNGMAVENGHVPQCHQKEP 1112
Db 444 -----SKLNTSKQALENQEPONKV-----PAEDLTLTFSDVPNGSALTQENISL 488
QY 1113 PKOKQSL 1120
Db 489 LSNKTISSL 496

RESULT 9

US-11-072-512-3665
 ; Sequence 3665, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOKIKO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKYU
 ; APPLICANT: NAGAHARA, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 08435-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3665
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-072-512-3665

Query Match

Best Local Similarity 34.1%; Pred. No. 2,3e-33;
 Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YYPPTVPAGVACVPRFVRSNNVPESSLPASMPYADHYSTFSPRDMSSPYQPPPP 677
 Db 2 YTPPP-----QCVRFRV---PPSAPPAPPYLDHYPPYL-QERVVNSQYGTQPO 49
 QY 678 QPYGVPPVPSGMYPVYNSRIRKMPMWQDDIIRNSLPPMDVMHSSV--YQTSLRER 735
 Db 50 Q---YPPI---YPSHYDGRVYPAPSYTRKEIFRESPI-PIEIPPAVPSVPSRER 100
 QY 726 YNSLDGYSVACQ---PS-----EPRTVPREPFCGLKTSCEQRKRPDQMAQYRT 787
 Db 101 YQGISYVVAHPPIQIRPSYRREPPYSKLP PPPQ---HSLDLRLHRRKREIMAQLEE 156
 QY 788 QKAPLVSTLPVATOSPPTPSPLFSVDFRADSESYSVGTKEFEDHLSHYSPWSCGTIGSC 847
 Db 157 RK---VISPPPA-PSPPLP-PTFHEBEFLDLDKAG-KYGNQVDSQSPWSCDTIGSY 210
 QY 848 INAISEPEPDVANSNAVLMDIDSGDVKKRVHLPFQRTKE--EDPIIPESDGPISKM 905
 Db 211 IGTKAKPDDVVAAGSVEMMNVESKGM--RDQRLDQRRAAFTSDDLIPFQDRPTVSRP 268
 QY 906 GAISRSRTGYHTTPOVQATASQGSATKDISVDVYPYNAVDSRW--SSYG--NEATSS 961
 Db 269 GAISTSKTIYTGAGPMQMAPQAGATKINSIDSPY--GTHGNGASPYSPHONIRPQ 326
 QY 962 AHYVERDREIVTDLGHRK--HSTGDLISLEIQ-----AKNSILLOR 1004
 Db 327 GHFSRERISMSVASHGKPLPSAEREQRLLEQLQINHQISOOTQLRGPEAVSNRLVLR 386

QY 1005 EANALAMQ-----KWSNIDEGRHLLTNT--LSKEIELRNGEIOSDYTEDATDKPD 1054

Db 387 EANTLAGSQPPPPPKPKPMISSEQLSELHQYREIRKTRRLSM--NCCSLDMK-- 443

QY 1055 RDIELLSALDTE--PDGQSEPIEBILDIQGISQNDQILNGAVENGHPVQHQKEB 1112

Db 444 -----SKLNTSKOAEHQPEPQNV-----PAEDTLTFSPDPNGSALTOENISL 488

QY 1113 PKQKKSL 1120

Db 489 LSNKTSSTL 496

RESULT 10

US-09-867-550-1346
 ; Sequence 1346, Application US/09867550
 ; Patent No. US20020082206A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Mehraban, Fuad.
 ; APPLICANT: Conley, Pamela
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Topper, James
 ; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
 ; FILE REFERENCE: 21402-013 (Cura-313)
 ; CURRENT APPLICATION NUMBER: US/09/867,550
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: USSN 60/208,427
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 2125
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1346
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-867-550-1346

Query Match

Best Local Similarity 7.9%; Score 490; DB 3; Length 95;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1097 MAVENGHPVQHQKEPPKQKQSLGPDHYILEEOKTILPVTSCFSQPLPVSISNASCPLP 1156

Db 1 MAVENGHPVQHQKEPPKQKQSLGPDHYILEEOKTILPVTSCFSQPLPVSISNASCPLP 60

QY 1157 TTSVAGNLLIKTHVMSDDKNDFLKPVANGKVVNS 1191

Db 61 TTSVAGNLLIKTHVMSDDKNDFLKPVANGKVVNS 95

RESULT 11

US-09-864-761-48290
 ; Sequence 48290, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Ranzel, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263,6
 ; PRIOR FILING DATE: 2000-10-04


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Db 213 ASDQKQEKPKDPVLKSPVLRLVLSEKK-----EQEGQTSFTTAIVSIAELPLRP 266
Qy 904 KKGAISSRSRTGYHTTDPVOATASQGSATKPISSVDYVPYNAVDSRWS-----'----- 952
Db 267 SPTTVSSVARS-----TIAAPTSSALSSQPI-----FTTAIDRCCLSSPREDTPI 313
Qy 953 ----SYGNEMTSSAHYVERRFI-----VTDLSG-HRHHSSITGDL 988
Db 314 PSLTCTETSDPLPTNENDDDICKPCSVAPNDIPLVSSTNLINEINGVSEKLSATESTIV 373
Qy 989 SHELQAKSNSLLQREAN-----ALAMQCKMNSLDEGRHJT 1025
Db 374 ELVKQEVL--PLTLELFINPREMKLEFIVPAATTVSSPSAALTQVRLER-DESIRRC 430
Qy 1026 LMLLSKEIFELRNGELQSD-YTEDADYT-----KP-DR----- 1055
Db 431 LSEDAKEIQ-NKIEVADQCTEEILDQSUNLSRSPVPAQIAITVPKTKWKKPDRTRTTE 489
Qy 1056 ---DIELELSALDTPEDPDQSEPIEILDIQGISQNDQNLNGMAVENGHPIQCHQKRP 1112
Db 490 EMLEAELELKA-----EBELSIDKVLSESDKMSQGF-----HP---ERDP 527
Qy 1113 PROKQSLGEDH 1124
Db 528 SLLKKVKAIVEN 539

RESULT 14
US-10-840-512-196
; Sequence 196, Application US/10840512
; Publication No. US20050125852A1
; GENERAL INFORMATION:
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: MANNING, GERARD
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: GRIGORIEV, IGOR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-1455
; CURRENT APPLICATION NUMBER: US/10/840,512
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469,014
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196
; LENGTH: 2377
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-840-512-196

Query Match 3.3%; Score 207; DB 5; Length 2377;
Best Local Similarity 19.3%; Pred. No. 0.00027;
Matches 216; Conservative 152; Mismatches 424; Indels 326; Gaps 46;

Qy 48 KACPFDQTAINT-----DIDYLPVYNALLQYGAQVPDQSTKLSNLGEN 92
Db 375 KASPFKSVIGTPEFNAPMEYEKYDESVDYVAFGCMLEMATSEYP----- 421
Qy 93 KHYEVAKKCEVDLALYLKPLSGKGVASINOSAL-----SRPMOKLVTLVN 139
Db 422 -----YSEQONAAQIYRRTVSGVK-PASFDKVAIIPVKKEIIISGCIKRONDERYSIMDLN 475
Qy 140 COLVEBEGVYRMPARASISGERTVTELLIOHQNPQOLSANLMAVARGCOFLGPMQOE 199
Db 476 HAFPEETEVRLAEEDDEGEKAITLMLRIEDIKLK-----GKYKDE 520
Qy 200 AKLVLLALEDSALSRYLVLFVQORLEPRFPAQAKSTIGHVQ-----LTYRAS 250
Db 521 AIEF-----STDERDYVEDVYAGQMVESGYVCEGDHKTAKAIDRVIS 563
Qy 251 CFKVTREDDSSIMQLKEEFRSYEALRRHDAQIVHIAEAGLRISPEQWSSILYGDLAN 310
Db 564 LTK-RREBGRQLVREGEKQKQESSFKQONEQOASVS-QAGI-----QLLSAASGTGIPTA 617

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Qy 311 KSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDNPANLNLRPHLELANIDNPDAVSP 370
Db 618 PATSASVSTQVPEPEPEADQHQQ-----LQYQPSISVLS--DGTIDGQGS 662
Qy 371 WEOLENAMAIVKTVVHGLVDPIQNSYRKQKET-----POPOKNSKYKTSMCRD 418
Db 663 SVFTESRVSQOTVSYG-----SQHEQAHSTGTAPRGHTVSSIQASQSOHQGYIPPSMAQ 716
Qy 419 LRQGGCCPRGTCPTFAHSGELEKYRLRNKKINATVTRFPLLN--KGVANNVTTTAGNV 476
Db 717 GQNGOQ-PSSSLAGVLSQ-----PIQHPQQQGIQPT----- 747
Qy 477 ISVISTETTKIIVSTGNSINAENSVSQILSRSTDSTIRALETVKVKVQKANGQNAAG 536
Db 748 -----VPSQAV-----QYSLPQAASS-----EG 767
Qy 537 PSADSVTENKIGSPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRVPVPPHSE 594
Db 768 TTAQPVSOQVSAQTOLPVSOIVATVQSEPHIIPVSTQPSVVVHSGAHLFPMQOPIPTSL 827
Qy 595 NIQYQDPRQTQIPFEVPOY--DQGYPPPTVPAQVACVPRFVRSNNVPSSSLPASM 652
Db 828 LPQY---PVSQIPRISTPHVSTAQTFSSVPTMAAGINQ--PLTLASATASSIIGSGSP 882
Qy 653 PYADHXT--FSPRDRMNSSPY-----QPPRPQYGPVP-----PVPSG--MYAPVD 696
Db 883 VVBNQLPTLLQPNVLOQSVHNPOLLQPTVQSIG-IPANLQGAABEGLPSGDVLVYG-PP 940
Qy 697 SRIRPMPYQRDIDIRNSLPRPDMVHSSVY--QTSLREYVNSLDGYVAVACOPSEPERT 755
Db 941 SR---LPQYQPDSSINAPSNVASCINHTVLAPRSMPEALATQCYFTTVQPYVESRP 997
Qy 756 TVPLPREPCGHLKTSCEEQIRKKPDQMAQYHTOKAPLVSS-----TL 797
Db 998 LVPM-GSVGQGVQVS-----QPAVSLTQPPPTSSQQAIVLESTQGVSAAPPEQT 1046
Qy 798 PVATQSPTRPSPLFS-----VDFRADPSH-----SVSGCTFEEDHLSHYSPWSGCTIG 845
Db 1047 PITQSQPQPVPLVTSADSAHSDVASGMSDGENAPSSGRHEGRTTKYHK--SVNS 1103
Qy 846 SCINAIDSEPKDVIAN-----SNAYLMDLSDGDVKKRYVLFTQRTKEDEP1IIPSDGP 900
Db 1104 RSRHEKTSRPKLRILVNSKGRVYVECOLETHNRKKNVTKFPDGDNPBEIATIMWNNDF 1163
Qy 901 IISKGAISRSS-----RTGYHTTDPVQ-----ATASQ 928
Db 1164 IL-----AIERESFVAQVREIIEKADEMUSEDEVSVPEBQGLESLQKDDYGFPGSQKLE 1219
Qy 929 GSATKPISSVDYVPYVNAVDSRWSSYGNATSSAHYVERDRIYVDSLGRKHSS---TG 985
Db 1220 GFFKQPIAVSSMPQOIGVPTS-----SLTVVHVSAGR-REIVSVPSRLESKVFYS 1271
Qy 986 DELS-LELQAKSNSLLQREBANALAMOOQKMSLDEGR 1022
Db 1272 DISDPRVASTSQAPGMNLSHSASSLQQAPESELKHGQ 1309

RESULT 15
US-11-096-568A-27756
; Sequence 27756, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27756
; LENGTH: 674
; TYPE: PRT

```


November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Db      181 LDSDSEETVRKGCOSVADQELLQAPQADGEG--KLHSAEBAACERFSEGRINLEHQ 238
Qy      300 WSSLLYGLAHKSHMOIITDKQSPESPAKSVQELTIVIQRTGDPAANLRAPHELLAN 359
Db      239 CSDDLNPTENHATE-----RHPEK--CQISISINVCPECGTDAHASISLPETSSLL 289
Qy      360 IDPNPDVAPPTWEQLENAMAVAKTVVGLVDFTQWYSR---KGHETPOPOPSKTKTSM 415
Db      230 IEDRNA-----EKAFCNKSQKPGIA--VSQSKMAAKGTCNDQVSTGKV-- 337
Qy      416 CRDLAQGGCGPRGTCTFAHQEELKRYLRNKKINATVTRPPLNKVGNNTVTTTAGN 475
Db      338 -----GPN--ADSLDERKW-----THP--QSLCPENSGATTDVP 368
Qy      476 VISVIGSTE-----TTGKIVPSTNGI-----SNAENSVQSLISTSTSTILAEITVK 523
Db      369 WITLNSVQKVNWESRTEMLTSDSARRHESNAEAIVLEVSNEVDG---GFSSSRK 425
Qy      524 VGKVG-----ANGONAAGPSADSVTENKIGSPPTKPVSNVATSAAGPSNVGTELS 574
Db      426 TLVLPDPHHTLMCKSGRPFKPEVDNISDKIFGKSYQKGR-----PHLH 473
Qy      575 VPQKSSPFLT--RVVYPPHSENIQYFQDPRTQIPEVPQYQYPPPTVPAG--V 629
Db      474 VTEIGTFITEPQITQEQPFTNKLKRRSTSLQPEDFIKKADAGVQRTPPDINOGTDL 533
Qy      630 AACVRFVANSNVVPSLSLPPACMPYADHSTSPRRMNSSPYQPPPPQYGVVPPVPSG 689
Db      534 ENEQAVSTTSCQEKIKIAGSNL--QKESKAHPESLKEP-----572
Qy      690 WYAPYDSRRIRMPWYQRDIIIRSNLSLPPMDV---MHSSVYQTSLEERYNSLDGYSA 746
Db      573 --ASTAGAST-----SNVSVDLEVLNVHSSKAPKRRLRKS-----SIR 612
Qy      747 COPPEPRTVPLPREPCHLKT---SCEEOIRRRPDQMAOYHTQKAPLVSTLPAVQ 802
Db      613 CALPLEPIRNPSP--PTCAELQIDSCSSEETKKNHNOQPAHLAEPOLIEDTEPAADA 671
Qy      803 SPTPSPPLFSVPFRADFSVSGTKEEDHLSHYSWSCGTIGSCINAIIDSEPKVIAN 862
Db      672 KNEBP-----BHRRR-----RAADAPFEELKMK 697
Qy      863 NAVLMDLSDGVKRVHLFETQRTKEBDPIIFPSDGLIISKWGAISRSGTYHTTDPV 922
Db      698 AGULITSCS-----PRKSQGPVN-----SFQRTTQGLR 729
Qy      923 QATAS-----QGSATKPIISVDYVYVNAVDSRMSSYGENEATSSAHYVERDR 969
Db      730 QMSDSAKELGDRVLGEPGKTTDRSEESTSVLS--DTDYDTQNSVSVLDAHTV---- 783
Qy      970 FIVTDLSGRKHSSTDDLSLELOAKNSLLQREANALMAQKNSLDEG-----RHL 1024
Db      784 -----RYARTSACQMTQFVASENPKELVHGSN-----NAGSGTEGKPLRLH- 826
Qy      1025 TINIISKEIENRGELOSQDYTE-----DATDTPKRDIDIELS 1062
Db      827 ALNLSQEKEMBESELDTOYLQNTFOVSKQSFALFSKRSRPOKCAHVSFSELEPKYT 886
Qy      1063 ALDTD--EPDQOSEPIEILDIQ-----LGISQNDQILNCAVENGHPV--QOHQKEP 1112
Db      887 AKGQKQERQOE--FEISHVQAVATVGLPVCQCGKLAADTMCRGCLCSSHYRS- 943
Qy      1113 PRQKQSLGSDHVIIEQKTIIPVTSQFQPLPVISNASCPLTTSVSAAGNLIKTHW 1172
Db      944 -----BENG--LSATGSGISQNSHFQ-----SVSPIRSI----- 973
Qy      1173 SEDKNDLKPVANGK 1187
Db      974 ---KTDNRKPLETGR 985

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US-11-293-697-3929
; Sequence 3929, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3929
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3929

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Query Match      2.8%; Score 171; DB 7; Length 577;
Best Local Similarity 22.0%; Pred. No. 0.016;
Matches 98; Conservative 50; Mismatches 147; Indels 150; Gaps 20;

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Qy      451 NATVTFPPLNKVGNNTVTTAGNVISVIGSTETTGKIVPSTNGISNAENSVQSLIS 510
Db      4 SASISM-----TGTIPPTTIKATGSTHTAPPTPTTSQSPSS---FSTA 50
Qy      511 TESTLALETYKVGKVGKVGANGONAGPSADSVTENKIGSPPTKPVSNVATSAAGPSNVGT 570
Db      51 KTSLSLPHNT-----SSTHPEVPTPTSTNTPKHTSTGTITPVAN--TTASASSRLPT 102
Qy      571 EV--NSVPQKSSPFLTRVNV-----YPPHSENIQYFQDPRTQIPEVPQY----- 613
Db      103 PFTTHSPFGSSPFGSTGWTATSPQTITTYTTPSH-----PQTLPTHVPFSTSLV 155
Qy      614 -----POTGYPPPTVPA-----627
Db      156 TPTHTVITTTHTQMATASISHTPTGVPPTTLKATSGTHTAPMTVTTSGTSHS 215
Qy      628 -GVAPCVPRFVNSN--VPE--SLPPAS-----MPADHYSTSPDRMNSPYOPPPQ 678
Db      216 FSTTASSFISSSWLPONSSSRPSSPTTQPLUSSATTVPSTTNQLSFSFSFSA 275
Qy      679 PYGVPVPSGMYAPYDERRIWRPWOYRBDIIRSNLSLPPMDVMSVYQTSLEERYNS 738
Db      276 PGTVSIVVPSHSSPQTS-----PVGNSGSFV--SAP-----VASTLLSGSHSLST 323
Qy      739 LDGYISVACP--PSEP-----RTTVPLPREPCHLKTSCEQIRKKPDQMAQYHTQK 790
Db      324 HPTTASVSASPLFPSSPAASTTIRATLP-----HTISS 356
Qy      791 PL-VSSTLPA--TOSPTPSPPLFS 812
Db      357 PFTLSALPLISTVTVSPSPSHLAS 381

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RESULT 3

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US-10-953-349-9275
; Sequence 9275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9275
; LENGTH: 3425
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

```


US-10-953-349-9275

Query Match 2.7%; Score 166.5; DB 6; Length 3429;
Best Local Similarity 19.2%; Pred. No. 0.33;
Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

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QY 247 YASCFKTKRDESSLMQKEEFSYEALREHDAQIYHIMEAGLRISPEQMSLLYG 306
DB 1190 YLESILRESKKEEDAPV--LDDDALNDLIARESEIDIFESIDKOKENEMETWNTLVHG 1247
QY 307 DLAKH-SHMOIITDKQSPESF-----AKVQELTIVLORT----- 341
DB 1248 PGSDSFAHIPSIRLVTEDDDKLYETMKNDVPVAAKESTVGMRKQSGMGLDTHQY 1307
QY 342 GDPANILNRLRPHLELLANID-----PNPDVSPTEQLENNAMVAVKTVHGLVDFIQ 394
DB 1308 GKGKRAEVRYSYEKLTBEFEKLCQTESPDSPQKGSESSSLADTNSIP-----VEN 1362
QY 395 YSRKGHEPQP-QPNSKYKTSKCRDLROQGGCPRGNTCTFAHQEELKYLKKNKINAT 453
DB 1363 SS-----DTLLPSPQAITVQGMPEVRPQ-----SHTLKEETQPIKRGGRPK----- 1406
QY 454 VTFPPLNKVGNVNTVTTTA-GNVISVIGSTETTKIVPSTNGISNAENSVSQILSRSD 512
DB 1407 -RTDKALTPVSLSAVSRTQATGNALS---SAATGLDFVSDKRLMAASHPTSLALTSFD 1462
QY 513 -----STLRALETYKVKGVANGQNAAG---PSADSVTENKIGSPPKT 553
DB 1463 LSGPFGFQSLPASPAFTPIRGGRGRSGRGAQRVGEVLHGNSISITQR----- 1514
QY 554 PVSNNAAATAGPSNVGTELSNVPQKSPFLTRVP-----VYPPHS----- 593
DB 1515 ---TETATSLADAEATKE-ALPRASAEIVSRVPKANEGSTSNPDQVSPHSAHTALRSD 1570
QY 594 -----ENIQYFODPRTQIPFEVPOYP-----QGYVPPPTVP----- 626
DB 1571 KAADKDLAPPGFDGSHVQTLNVLENSEBRKAFVKKRPLIQGVSSQHPGPKQPLDLP 1630
QY 627 -----AGVACPVPFVRSNNVPESSLPASMPY-ADHYSTFSPDR---MNSSPYQ-- 673
DB 1631 VSTSSITLGGGVQONAVSVCDGSKSPSEGRITYALQGVTTAPBDATLPMSSQGS DAT 1690
QY 674 -PPPOPYGP-----VPPVSGMYAVYDSRRIRWRPMPY---QRDDIIRNSLPPM 720
DB 1691 LPMSSQPVGSTVEAQEANVPSLPALPA---KRRVRNLPSRGETPCKRQKRGQPLPAT 1746
QY 721 DVNHSVVOGTSL---RERYNSLIDG---YGSVACQPSSEPRTTVLPREPCHLTSCE 772
DB 1747 DA--SSASTGLTPQILEVKVGNLSTKAKAFDAVAKQPHFSQVA-----PDHSSGSLS 1799
QY 773 EOIRR-----KPDQWAOYHTOKAPLVYSTLPVATQSPTRPSP- 809
DB 1800 QEIRHDTSGTSGSARKQTDVTVARVMKEIPSESTLKHKGEPATRTTNVPDAQSPG 1859
QY 810 ---LSVDRAPRSEVSQTFEE-----DHLSHYSPMCCGTTGSCINADSE 854
DB 1860 ENMLHVEVTHK--AEDSSGLKQOEALYNLSKADKLVSIDPHVPFGDLTSSGSVAN----- 1912
QY 855 PPOVANSNAV---LMDLSDGVKRVY---HLFET-----QRRTKEE 890
DB 1913 -KDVIGSSKVAENELVKIPGADVDSVITQSLGTLTTRAKSSLEKCTADQLGKLSQE 1971
QY 891 DRIIPESDPIISKMGALISRSRTGYHTDPVOATQASQASATKPIVSVDVPPYNAVDSR 950
DB 1972 GETTPASDETCHL--AEETASLSYVRBP---TASASTTAEPRLPTDLKKNISFQDE- 2025
QY 951 WSSYGNHATSSAHYVRDRFIYITDLSGHRKHSSTGGLLSLEQOASNSLLOREANALA 1010
DB 2026 -----YKTLNGDKREAL---LLSSE--EQTWNNSKI---ETNSSE 2057
QY 1011 MOOKWNSLDEGRHLTLNLISKEITELNGELOS DYTEDATDTKPDRIELELSALDDEPD 1070
DB 2058 LQA--SRDVEPHVD---GKSVYDANQYVKED-----EAKHSVEITQSSMLFEDLEP 2103
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QY 1071 GQSEPIEETLDIQ-LGISQNDQLANGMAVENGHPVQHQKPEPKOKKOSLGEDHYILE 1129
DB 2104 NAGQKHSSIDIQPIVLYTISNE---NANSLD-----KQYDPIRSKADIRQD----- 2147
QY 1130 QKTLIPVTSQFQOPLPVSTISNASCLPITTSVAGN---LILKTVHVSSEKDNPLKFPVANG 1186
DB 2148 -----PEESVFQV---GVGRPKVGTADTQMEDTNDAKLIVGCSVSESEKTKLQSLIFG 2198
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RESULT 4

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US-10-953-349-9274
; Sequence 9274, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9274
; LENGTH: 3438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9274
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Query Match 2.7%; Score 166.5; DB 6; Length 3438;
Best Local Similarity 19.2%; Pred. No. 0.33;
Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

```
QY 247 YASCFKTKRDESSLMQKEEFSYEALREHDAQIYHIMEAGLRISPEQMSLLYG 306
DB 1199 YLESILRESKKEEDAPV--LDDDALNDLIARESEIDIFESIDKOKENEMETWNTLVHG 1256
QY 307 DLAKH-SHMOIITDKQSPESF-----AKVQELTIVLORT----- 341
DB 1257 PGSDSFAHIPSIRLVTEDDDKLYETMKNDVPVAAKESTVGMRKQSGMGLDTHQY 1316
QY 342 GDPANILNRLRPHLELLANID-----PNPDVSPTEQLENNAMVAVKTVHGLVDFIQ 394
DB 1317 GKGKRAEVRYSYEKLTBEFEKLCQTESPDSPQKGSESSSLADTNSIP-----VEN 1371
QY 395 YSRKGHEPQP-QPNSKYKTSKCRDLROQGGCPRGNTCTFAHQEELKYLKKNKINAT 453
DB 1372 SS-----DTLLPSPQAITVQGMPEVRPQ-----SHTLKEETQPIKRGGRPK----- 1415
QY 454 VTFPPLNKVGNVNTVTTTA-GNVISVIGSTETTKIVPSTNGISNAENSVSQILSRSD 512
DB 1416 -RTDKALTPVSLSAVSRTQATGNALS---SAATGLDFVSDKRLMAASHPTSLALTSFD 1471
QY 513 -----STLRALETYKVKGVANGQNAAG---PSADSVTENKIGSPPKT 553
DB 1472 LSGPFGFQSLPASPAFTPIRGGRGRSGRGAQRVGEVLHGNSISITQR----- 1523
QY 554 PVSNNAAATAGPSNVGTELSNVPQKSPFLTRVP-----VYPPHS----- 593
DB 1524 ---TETATSLADAEATKE-ALPRASAEIVSRVPKANEGSTSNPDQVSPHSAHTALRSD 1579
QY 594 -----ENIQYFODPRTQIPFEVPOYP-----QGYVPPPTVP----- 626
DB 1580 KAADKDLAPPGFDGSHVQTLNVLENSEBRKAFVKKRPLIQGVSSQHPGPKQPLDLP 1639
QY 627 -----AGVACPVPFVRSNNVPESSLPASMPY-ADHYSTFSPDR---MNSSPYQ-- 673
DB 1640 VSTSSITLGGGVQONAVSVCDGSKSPSEGRITYALQGVTTAPBDATLPMSSQGS DAT 1699
QY 674 -PPPOPYGP-----VPPVSGMYAVYDSRRIRWRPMPY---QRDDIIRNSLPPM 720
DB 1700 LPMSSQPVGSTVEAQEANVPSLPALPA---KRRVRNLPSRGETPCKRQKRGQPLPAT 1755
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Qy 721 DVMHSSVYQTSI-----RRRNSLIDG-----YYSVACOPSEPRRTVPLPREPCGHLKTSCE 772
Db 1756 DA--SSASTGTLTPOIEVKVGNLSGTAKAFDAVAEQPHFSQSA-----PIHSSGSLIS 1808
Qy 773 EQIRR-----KPDQMAQYHTQKAPLVSSSTLPAVATGSPTRPPSP- 809
Db 1809 QEIRRDTSCTGSGARKQTADVTVARVMKEIFSETSLKHKGKGEPSATRTTVPPAQSPG 1868
Qy 810 ---LFSVDFRADFSSSVSGTKFEE-----DHLSHYSPMSCGTTGSCINAIABSE 854
Db 1869 EMLNLTVEITHK--AEDSSGLKNQOEALYNLSKADKLVSDFPHFVPGDGLTSSGSVAN----- 1921
Qy 855 PKDVANSNAV-----LMDLDSGDYKRRV--HLFET-----QORTKEE 890
Db 1922 -KDVIDGSSKVAENELVKIPGQDVDSVYQLSLGNTLTKAKSLSEKCTADQLLGEKLSQE 1980
Qy 891 DPLIFPSDGPILISKMGALSRSSRTGHTTDPVOATASQGSATKPLISVSDYVYVNAVDSR 950
Db 1981 GETTPASDGETCHL--AEETASLSLVSRSEF--TASASTTAEPPLPTDKLEKNISFQDE- 2034
Qy 951 MSSYGNENATSSAHYVERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLOREANALA 1010
Db 2035 -----VKTUNGDKRRAI--LSSB-EQTNVNSKI--ETNSBE 2066
Qy 1011 MOOKMNSLDEGRHLTLNLSKEIEIRNGELQSDYTEDATDTKPRDIELELSALDTPDEP 1070
Db 2067 LQA--SRDVEPHVD---GKSVVANQTVKED-----EAKSVELQSSMLPEDELIP 2112
Qy 1071 GQSEPIEELIDIQ-LGISSQNDQLNGAVENGHPVOHQKPPROKKSLOEDHYILEE 1129
Db 2113 NAGQKGHSIDIQPLVLTYSNE--NAMSILD-----KQYDPLISKADIDQD----- 2156
Qy 1130 QCTILPVTSCFSQPLPVISISNASCLPITTSVSGN--LILKTHVSEDKNDPLKRVANG 1186
Db 2157 ---PEESVFOV---GVGRPKVGTADTQMEDTNDAKLLVGCVSSESEKEXTLOSLIPG 2207

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RESULT 5

```

US-10-953-349-9273
; Sequence 9273; Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9273
; LENGTH: 3478
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9273

```

Query Match 2.7%; Score 166.5; DB 6; Length 3478;

Beet Local Similarity 19.2%; Pred. No. 0.34;

Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

```

Qy 247 YRASCFTKTRDESSLMQKEFRSYEARLRERHDAQIVHAMEAGLRISPEQWSSLLYG 306
Db 1239 YLESLRRESKKEEDAV--LDDDALNDLILARRESEIDIPESIDQKQENMEMETWMTLVHG 1296
Qy 307 DLAHK-SHMOSITDKQSPESF-----AKSVEELITVLORT----- 341
Db 1297 POSDSFAHPIPSIRLVTEDDLKLVTETKLVNDVPMVAKESTVGMKRRKQSGMGLDTHQY 1356
Qy 342 GDPANLNRIRPHILANID-----PNPDAYSPTMEQLENAAMVAVKTVHGLVDVFION 394
Db 1357 GNGKARARERYSERKLTBEFEKLCCTESPDSPQGGSGESKLANDTSNIP-----VEN 1411
Qy 395 YSRKGHTPOP-QPNRSKYTSMCRDLRQGGCPRGNTCTFAHSQEBLEKYLKNNKKNAT 453

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Db 1412 SS-----DTLLPFSPTQALTVQPMEEVRPQ-----SHTLKEETQPIKRGRRPK----- 1455
Qy 454 VRTPELKNKGVNNVTTTA-GNIVSVIGSTETTKIIPSTNGISMANSVSOLLRSRD 512
Db 1456 -RTDKALTPVSLSAVSRTQATGNALS--SAATGLDFPSSDKRLPAASHPTSLSLTSPD 1511
Qy 513 -----STLRALETVKVQKVGANQONAG--PSADSVTENKIGSPKPT 553
Db 1512 LSGPRGFSQSLPASPAPTPIRGGGRGRSRGRGARRRVEGLVHGSNSITQK----- 1563
Qy 554 PVSNAATSGAGSVNGTEILNSVPQKSPPLTRVP-----VYPPHS----- 593
Db 1564 ---TETATSLASDAEATKF-ALPRGASEIVSRVPRPANGSTSNPDQSVSHSATTALRSD 1619
Qy 594 -----ENIQYQDPRTOQPFVEVPQV-----QNGYVPPPTVP----- 626
Db 1620 KAADKDLAPGFGDSGHVQTLNLVNSSERKAFVKKRPLIQVSSQHFGKRNQPLDLP 1679
Qy 627 -----AGVAPCVPRFVRSNNVPSSSLPPASMPY-ADHYSTFSPDR--MNSSPYQ-- 673
Db 1680 VSTSTLLGCGFVQONQNAVSSVCDGSKSPSEGRITTLAQVTTAPSDATLPMSSQPSDAT 1739
Qy 674 -PPPOPYGP-----VPPVSGMYAPVYDSRIIMRPPMY-----QRDDITRNSLPPM 720
Db 1740 LPMSSQPVGSTVEAQEAVNPSPILPALPA---KREVRNLPKGETPKRQKRRGQPLPAT 1795
Qy 721 DVMHSSVYQTSI-----RRRNSLIDG-----YYSVACOPSEPRRTVPLPREPCGHLKTSCE 772
Db 1796 DA--SSASTGTLTPOIEVKVGNLSGTAKAFDAVAEQPHFSQSA-----PIHSSGSLIS 1848
Qy 773 EQIRR-----KPDQMAQYHTQKAPLVSSSTLPAVATGSPTRPPSP- 809
Db 1849 QEIRRDTSCTGSGARKQTADVTVARVMKEIFSETSLKHKGKGEPSATRTTVPPAQSPG 1908
Qy 810 ---LFSVDFRADFSSSVSGTKFEE-----DHLSHYSPMSCGTTGSCINAIABSE 854
Db 1909 EMLNLTVEITHK--AEDSSGLKNQOEALYNLSKADKLVSDFPHFVPGDGLTSSGSVAN----- 1961
Qy 855 PKDVANSNAV-----LMDLDSGDYKRRV--HLFET-----QORTKEE 890
Db 1962 -KDVOIGSSKVAENELVKIPGQDVDSVYQLSLGNTLTKAKSLSEKCTADQLLGEKLSQE 2020
Qy 891 DPLIFPSDGPILISKMGALSRSSRTGHTTDPVOATASQGSATKPLISVSDYVYVNAVDSR 950
Db 2021 GETTPASDGETCHL--AEETASLSLVSRSEF--TASASTTAEPPLPTDKLEKNISFQDE- 2074
Qy 951 MSSYGNENATSSAHYVERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLOREANALA 1010
Db 2075 -----VKTUNGDKRRAI--LSSB-EQTNVNSKI--ETNSBE 2106
Qy 1011 MOOKMNSLDEGRHLTLNLSKEIEIRNGELQSDYTEDATDTKPRDIELELSALDTPDEP 1070
Db 2107 LQA--SRDVEPHVD---GKSVVANQTVKED-----EAKSVELQSSMLPEDELIP 2152
Qy 1071 GQSEPIEELIDIQ-LGISSQNDQLNGAVENGHPVOHQKPPROKKSLOEDHYILEE 1129
Db 2153 NAGQKGHSIDIQPLVLTYSNE--NAMSILD-----KQYDPLISKADIDQD----- 2196
Qy 1130 QCTILPVTSCFSQPLPVISISNASCLPITTSVSGN--LILKTHVSEDKNDPLKRVANG 1186
Db 2197 ---PEESVFOV---GVGRPKVGTADTQMEDTNDAKLLVGCVSSESEKEXTLOSLIPG 2247

```

RESULT 6

```

US-10-559-415-190
; Sequence 190; Application US/10559415
; Publication No. US20060100132A1
; GENERAL INFORMATION:
; APPLICANT: Astrazeneca AB et al
; TITLE OF INVENTION: Diagnostic Method
; FILE REFERENCE: 101073-IP WO
; CURRENT APPLICATION NUMBER: US/10/559,415

```

CURRENT FILING DATE: 2005-12-06
 PRIOR APPLICATION NUMBER: 0313081.2
 PRIOR FILING DATE: 2003-06-06
 NUMBER OF SEQ ID NOS: 191
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 190
 LENGTH: 1809
 TYPE: PRT
 ORGANISM: Homo Sapiens - peptide sequence of amino acids
 US-10-559-415-190

Query Match 2.6%; Score 159.5; DB 6; Length 1809;
 Best Local Similarity 19.1%; Pred. No. 0.33;
 Matches 246; Conservative 174; Mismatches 429; Indels 437; Gaps 66;

```

QY 48 KACPDDQAINIDIVLPVNFALLQVGAQVDPDHQSIKLSNGENHGYVAKKCVEDLAL 107
DB 351 KSTSEKKAANEEMAL-----RQIKD--TVTMDAGRANKEVEILRKQCALCO 397
QY 108 YKPLSGGKVASLNS-----ALSRPMQRKLVTLVNCQVVEEGRVRA--RA 154
DB 398 ELKEALQADVAKCRDMAFOERDKIVARDSIRTL-----CDNLRR--RDRAVSELABA 451
QY 155 ARSLGE-----RTVTEILQHQNPQOLSANMAAVRAGCQFLGPAMOEALKVLV 205
DB 452 LKSLDTRKQKNDVRELKEL-----KQMESQLEKEARFR--QLMAHSHDSALDIDS 503
QY 206 LALE-----DGSALSRKVLVLFVYQRL--EPRPQ-----ASKTSIGHVVQLVLRASC 251
DB 504 MEMETEVEFERETEDIDIKALGFDMAGVNEPCFGDCGIFVTYKDKGSIDAGRLRVND 563
QY 252 FVYTRKDESSLMOLKEERSEYAL-----RREHDAQIV--HIAM---EA 291
DB 564 WLIRINDV--LINDKKQALKALINGGAINMVRRKKSIGKVVTLPHLNLSCQKDS 620
QY 292 GLRISPEQW--SSLYXDILAKHSMOSIIDLKQSPESFA---KSVQELTIVLQRTGDPANL 347
DB 621 GISELGVAAAVLPSSPAKESGLAVGDRIVAINIADNKSINCESLIRSCQDSLT 680
QY 348 NLRPLHLLANIDPNDAVSPTQELNAMAVALKTVHGLVDLFIONYSRKGHETPOPOP 407
DB 681 SILK-----VFPO-----SSSW-----SGQNIENIKQSDKMLSFRAH--GREVOA 719
QY 408 NKR-----YKTSKCRDLRQGGCGPRGNTCFPAISQELKRYLRANKINAT 453
DB 720 HKRKLIOHNNSTQTDIFYTDLERKEGC--PPGSSSFLH----- 759
QY 454 VRTPLANKVGNNTVTAGNVISVIGSTETTGKIVPSTNGISNANGSOLISRTDS 513
DB 760 -KPPF-----GGPLQVCPOACPSA-----SERLSFRSDASGD 792
QY 514 TLRALETYK-----KVGKVGANGQNAAGPSADSVTEKNGISPKPTPVSNVAATSA 563
DB 793 RGFGLVDVGRRLPLPFETEVGPGCVG--EASLDKADSGSNGCGTWPFAMLSSTA----- 846
QY 564 GGSNNGTELNSPQKSSPFLTRPVYPPRSENIQYQDRTQIQPEVPOY--POTGV----- 618
DB 847 -----VPEKLS-----YKKPKRKSIF--DENT--FKRPQTPPKIDILPBG 884
QY 619 -----YPPPTVPAG--VAPCVPRFVNSNV-----PESSLP 648
DB 885 PEPAPSPQSKAGAPLTPPKPRR--RSDSIKFOHLETSESEBATTVGSSPSTSPSALP 942
QY 649 P-----ASNPYADHYSTFSP-----RDR 666
DB 943 PVDVCEPMAHAPPRKARVRIASSYYPEDGDSSHLPAAKSCDEDLTSGKVDLQGRRR 1002
QY 667 MNSSP--YQP-----PPQPYGPPVPSPGMYAPVYSRRI 700
DB 1003 PKSASBFRKLAPVVIIPAQLEBQKVPASGELSPLOEMAP-----YSGHSSRRS 1054
QY 701 WRPPMYQDDIIRSNSLPMDVHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLP 760

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DB 1055 -NPPLYPSR-----SVGTVPRLSTPTTTS$ILLNPIYTVRSHRVGCPSSPAPADAGPQG 1110
QY 761 REPCHLTKTSCBEOIRKRPD-----QMAQYHTQAKAPLVSTLPVATQSPTRPSLFSVDPR 816
DB 1111 LHP-----SVQHOGSLTDLSHRTCSDYSEMRATGNSLPSASRLGSSS-----NLQFK 1160
QY 817 AD-----PSESVGTKFEEDHLSH-----YSPWSCGIGSCINADSE-----PKD 857
DB 1161 AERIKPTSTPRYPRSVGS--ERGSVSHSECTPPQSPPLNIDTSSCSQSQTASLFR-- 1217
QY 858 VIANSNAVLMDLSDGVKRRVHLFETQRTKEEDPIIPF-----SDGPILSKWGAIS 909
DB 1218 -IANNPASI-----GERRRDRPYVEEPRHYKVGKSEPLGISIVSEKGGIYVSKTVGS 1271
QY 910 RSRRTGYHTTDPV-----QATASQ-----GSATKPIYV--SDYPPVYNAVDSRWSSY 954
DB 1272 IAHQAGLEYGDDOLLEENGINLRSAEQOARLIIGQCCDPTTTLAQVNPYHQLSS----- 1326
QY 955 GNEATSSAHYVERDRITVTDLSGHR--KHSTGDLTSLLEQO-----AKSNGLLQREA 1006
DB 1327 --HSRSSHLDPAGTHSTLQSGGTTTPHRPSVIDPL--MEQDEGPTTPPAQSSRLAGDA 1383
QY 1007 NALAMQO-----KMSLDEGRHLTLNLSKETELRNGELQSDYTEDATDTKPPDR----- 1055
DB 1384 NKKTLEPRVFIKKQSLGELGVHL-----CGNLHGVAVEVEDSPAKGPDGLV 1432
QY 1056 --DIELESLADTDEPDQSQSEPIEET 1079
DB 1433 PGDLILEYGLSDV-----RNKTVEEV 1453

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RESULT 7

US-10-559-415-2
 ; Sequence 2, Application US/10559415
 ; Publication No. US20060100132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Astazeneca AB et al
 ; TITLE OF INVENTION: Diagnostic Method
 ; FILE REFERENCE: 101073-1P WO
 ; CURRENT APPLICATION NUMBER: US/10/559,415
 ; CURRENT FILING DATE: 2005-12-06
 ; PRIOR APPLICATION NUMBER: 0313081.2
 ; PRIOR FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 1919
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-559-415-2

Query Match 2.6%; Score 159.5; DB 6; Length 1919;
 Best Local Similarity 19.1%; Pred. No. 0.36;
 Matches 246; Conservative 174; Mismatches 429; Indels 437; Gaps 66;

```

QY 48 KACPDDQAINIDIVLPVNFALLQVGAQVDPDHQSIKLSNGENHGYVAKKCVEDLAL 107
DB 461 KSTSEKKAANEEMAL-----RQIKD--TVTMDAGRANKEVEILRKQCALCO 507
QY 108 YKPLSGGKVASLNS-----ALSRPMQRKLVTLVNCQVVEEGRVRA--RA 154
DB 508 ELKEALQADVAKCRDMAFOERDKIVARDSIRTL-----CDNLRR--RDRAVSELABA 561
QY 155 ARSLGE-----RTVTEILQHQNPQOLSANMAAVRAGCQFLGPAMOEALKVLV 205
DB 562 LKSLDTRKQKNDVRELKEL-----KQMESQLEKEARFR--QLMAHSHDSALDIDS 613
QY 206 LALE-----DGSALSRKVLVLFVYQRL--EPRPQ-----ASKTSIGHVVQLVLRASC 251
DB 614 MEMETEVEFERETEDIDIKALGFDMAGVNEPCFGDCGIFVTYKDKGSIDAGRLRVND 673
QY 252 FVYTRKDESSLMOLKEERSEYAL-----RREHDAQIV--HIAM---EA 291

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Db 674 WLLRINDV---LINKDKQAIIKALLNGEAIINWVRKRKSLGKVITPLHINLSGQKOS 730
Qy 292 GLRISPEQW--SSLVGLDLAKHSMOSIIDKOSPESFA---KSVDELITVLORTDPAUL 347
Db 731 GISTENGVAAAVLPGSPPAKESGLAVGRIVAINGIALDNKSLNECESLSCCOQSLTL 790
Qy 348 NLRPLHLELIANIIDNPDAVSPTEWOLEENAMAVAVITVHGLVDVFIQNSRKGHETPOPOP 407
Db 791 SILK-----VFPQ-----SSSW-----SGQNFENIDSDKMSLFRAH--GREVQA 829
Qy 408 NSK-----YKSMCRDLRQGGCGPRGTNCTFASQEBLEKYLRLNKKINAT 453
Db 830 HMKRMILIOHNNSTQDIFPYTDLERKEBEG--PPGSSSFFLH-----869
Qy 454 VTFPLLNKVGNNVTTAGNVISIGSTETTGKIVPTNGISNAENVSQILSRSTDS 513
Db 870 -KPPF-----GGPLQVCPQACPSA-----SENSLSFRSDASGD 902
Qy 514 TLRALETYK-----KVGKVGAMGQMAAGPSADSVTENKIGSPKTPVSNVAATSA 563
Db 903 RFGGLVDVGRRRPLPFETEVGPCVG--EASLDKADSGSNSGGTWPKAMLSSTA-----956
Qy 564 GPSNVGTBLNSVPQKSSPFLTPVVPYPHSENIQTFQDPRTOI PREVPQY--PQTGY----618
Db 957 -----VPEKLS-----YKKPKORKSIF--DENT--FKRPQTPEKIDYLLPG 994
Qy 619 ----YPPPTVAG--VAPCVPRFVRSNNV-----PRESSLP 648
Db 995 PGPAHSPQDSKRAGPLTPPKPR--RSDSIKFOHRLTSESEBAILVGSSTSPSALP 1052
Qy 649 P-----ASNRYADHYSTFSP-----RDR 666
Db 1053 PVDVGEPMHASPRAKARVRIASSYVPEGDGSHLPAKKSCEDELTSQKVDLQKRR 1112
Qy 667 MNSSP-YQP-----PPQYGVPRPVPSGMAYAVYNSRI 700
Db 1113 PKSASFPKLAIPVYI PAQLEBQKCPVPSGELSPLQEMAP-----YSGHSSRS 1164
Qy 701 WPPMWQRDIIIRSNLPRMDVHMSVQTSIRERNNSLDGYVSVACQPPSEERTVPP 760
Db 1165 -NPILYPSRP--SVGTVPRLSLPTTSVSLBNPIYTVRSHRVGVCSSPPAARDGPG 1220
Qy 761 RPPCGHLKTSCEBQIRKPD-----QMAQYHTOKAPLVSTLPVATQSPTPPSLFSVDR 816
Db 1221 LHP-----SVQHQRSLSLDLSHRTCSQDSEMRATGNSNSLPESARLGSS--NLQPK 1270
Qy 817 AD-----FSESISGTFEEDHLSH-----YSPMSCGTIGCINAIDSE--PKD 857
Db 1271 AERIKIPSTPRYPRSVVGS--ERGSVSHSECTPPQSPPLNIDTLSSCSQSQTSASTLPR- 1327
Qy 856 VIANSAVIMDLDSGDVKKRVHLFETQRTKEEDPIIFP-----SDGPIISKWGAIS 909
Db 1328 -IAVNBASL-----GERRKDRPVEPRVAVKQKSEPIGISTVSEKGIYVSKTVGS 1381
Qy 910 RSSRTGYHTTDPV-----QATASQ-----GSATKPIV--SDVYPVNAVDSRWSY 954
Db 1382 IAHQGLEYGDDOLEFENGINLSATEQOARLIIQQCCDTITIAQVNPVHQSS-----1436
Qy 955 GNEATSSAYVERDRITVDSLGR--KISSTDLSLEIQ-----AKSNLLIQREA 1006
Db 1437 --HSRSSHLDPAGSTHSTLQSGSTTPPHPSVIDPL--MEQDEGPSTPPAKQSSRIAGA 1493
Qy 1007 NALAMQ-----KMSGLDEGRHLTLNLKSKEILRNGELQSDYTEDATGTPKPR-----1055
Db 1494 NKKTLEPRVFTIKSQLEIGVHLC-----GNNLHGVVAVEEDSPAKGPDGLV 1542
Qy 1056 --DIELESLALDTEPDQSEPIEET 1079
Db 1543 PGDLILEYGLDY-----KMKVIEEV 1563

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RESULT 8
US-11-293-697-3230

```

; Sequence 3230, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 3230
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3230

```

Query Match 2.6%; Score 159; DB 7; Length 1057;
Best Local Similarity 19.6%; Pred. No. 0.17;
Matches 146; Conservative 100; Mismatches 264; Indels 234; Gaps 36;

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Qy 554 PVSNTVAATSA-----GPSNVGTBLNS-----V 575
Db 3 PLSVAYSTSAKNDLNLRSQTGKCHLHRHFPVDVPLNQLQRPPOETGERLNKYEENRI 62
Qy 576 PQKS---SPFLTRVPVYPHSENIQYF---ODPRTOI-----PFEVP 611
Db 63 LOESIDVAFPTTKIKIGLEBERENYSRVASSSPKSHIIKQMDVRSVSLDKMHGHSVP 122
Qy 612 Q-YPQTGYVPPPTVAGVAPCVPRFVRSNNVPESSLPPASNP-----YADHYSTFSP 663
Db 123 QSLPQSNVPT-----TLSNSVYNE--PPRSYPSKEVSNIIYGKQSNALA 164
Qy 664 RDRMN-----SSPYQPP--PQYGVPRPVSGWAP-----YDSRRIRWRPM 705
Db 165 AAAAPQTLTSTTSISKRPPLIKHQPESVEGKIE--HLPHQASHSVTTRNDCRSPT 222
Qy 706 YORDIIRSNLPRMDVHMSVQTSIRERNNSLDGYVSVACQPPS-----751
Db 223 HL--TVSSNTILRSMPLHRAVFPFRIHLSLEKEGASIS--SLSPFLTPVWPVNAQKV 279
Qy 752 ----EBRITVPLPREPCGHLKTSCEBQIRKPDQW-----AQYHTOK-----AP 791
Db 280 QSQKRPPLIPPKDSQANFKSSSEQSL--TEMWRPNNNLSKEKTEHVEKSSGKLQAA 336
Qy 792 LVSTLPVATQSPTPPSLFSVDRADPSEBVSCTFEEDHLSHVPMSCGTIGCINAI 851
Db 337 MASVIVRPSSSTKTDSPMAQOLASKDVRSESSAGAHKTDCLKLAEGETGRI--ILPNV 394
Qy 852 DSEPKDVIANSAVIMDLDSGDVKKRV--HLFETQRTKEEDPIIFPSDGPILSKWGAISR 910
Db 395 NBD--SVHTKSEKNPOAVSQGSVPSSVMAVNTMCTK--TDVITSAADTTSVSSWG--448
Qy 911 SSRTGYHTTDPVQATASQGSATKPIIS-----VSDYVPVNAVDSRWSYGEATS 960
Db 449 SEVTSLSNLTILASTSECEVSSKSVSQPAVQKQCKVSTTAPVTLAS--SKTGSVVOP 504
Qy 961 SAHYVERDRFITVDSLGRHKHSGSTGDLLELQOAKNSLLQREANALAMQKMSLDE 1020
Db 505 SSGFSG--TTDFILHLKHKHA-----ALAAQYSSN--ASTETBNALIKNQLASLPL 553
Qy 1021 GHMLTLNLKSKEILRNGELQSDYTEDATGTPKPRDRIEELSAL-----DTDEPDQ 1072
Db 554 DSTVICSTINKANSVANGQA-----SQTSQPNYHTKLKKMWLTHSEEDKNTNKGNS 606
Qy 1073 SEPIEBIL-----DIQGISQ-----NDQLN-----GMA 1098
Db 607 GMSVSEIIRKPSVNLIASTSDIQNSVDKSIIVDKVYKVRRAKRTYESGESGDS 666
Qy 1099 VENGHPVOQHOKEPKK---QKKOS 1119
Db 667 DESEKSEQRTKRPKPYKKON 690

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RESULT 9
US-10-953-349-13469
; Sequence 13469, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13469
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13469

Query Match          2.6%; Score 158.5; DB 6; Length 443;
Best Local Similarity 21.5%; Pred. No. 0.054;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTRTFPLNKVGVNNVTYTTAGNVISVIGSTETTGKIVPST 493
DB 67 AETQKELAKQLAQKSSS-----SS 87
QY 494 NGISNAENSVSQLISRSTDTSLRALETYKVGKVGANGQ-----NAAGPSA 539
DB 88 HSQSNBESSPTTDPKKTDNA-----SDANNQALALPHQIAPQPPAAPS 135
QY 540 DSVTENKIGSP-----PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLTRVPY 589
DB 136 QAAASNVTQAPQPPYYIIPPTMPN-SALPHQHQNQLPSDQYRTPQLVAPQPTPSQVT 194
QY 590 P-PHSENTIOYFODPRTQIPFEVPOYPTGY-----YPP-----PTVPAGVAPCVR 635
DB 195 PSPPVQGFSHYQPPQQ-QQPPQQQQQQSQOVQPSQPPMOSQVRPSSPNVYPPYQPN 252
QY 636 FVRSNNVPESSSLPPASMPYADHYSTFSR--DRMNSSPY-----QPPPPQPYGP 682
DB 253 --QATNPSPAETLPSNMANQMPYSGVPPQGSNRADAIPIGYGAGRTVPQPPQMKSS 310
QY 683 VPPVSGMTAPYDSSRIWRPMPYQRDIIIRNSNLPMDVMHSSVYQTSIRERYNSLDGY 742
DB 311 FPAPPGEMVGP-----TGSLLPALPPSSA-----YMMYDGE 341
QY 743 YSVACQPPSEPR-----TTVPLPREPCGHLKTSCEQIRRKPD--QMAQYHTQKAPL 792
DB 342 GGRSHHPQPPPHAPQPGYPTTSASLONPPQH-----NLMTANPQSQFVRNHPNELI 395
QY 793 VSSITLVATQSTPPSPPLFSVDPRADFSSVSGTKFE-----DHLSHYSP--- 838
DB 396 -----EKLVMGFRGDHVASVI-QRMESGQAVDFNSVLDRLSSVGPQRG 439
QY 839 -WS 840
DB 440 GWS 442

RESULT 10
US-10-953-349-13468
; Sequence 13468, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30

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; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13468
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13468

Query Match          2.6%; Score 158.5; DB 6; Length 451;
Best Local Similarity 21.5%; Pred. No. 0.056;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTRTFPLNKVGVNNVTYTTAGNVISVIGSTETTGKIVPST 493
DB 75 AETQKELAKQLAQKSSS-----SS 95
QY 494 NGISNAENSVSQLISRSTDTSLRALETYKVGKVGANGQ-----NAAGPSA 539
DB 96 HSQSNBESSPTTDPKKTDNA-----SDANNQALALPHQIAPQPPAAPS 143
QY 540 DSVTENKIGSP-----PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLTRVPY 589
DB 144 QAAASNVTQAPQPPYYIIPPTMPN-SALPHQHQNQLPSDQYRTPQLVAPQPTPSQVT 202
QY 590 P-PHSENTIOYFODPRTQIPFEVPOYPTGY-----YPP-----PTVPAGVAPCVR 635
DB 203 PSPPVQGFSHYQPPQQ-QQPPQQQQQQSQOVQPSQPPMOSQVRPSSPNVYPPYQPN 260
QY 636 FVRSNNVPESSSLPPASMPYADHYSTFSR--DRMNSSPY-----QPPPPQPYGP 682
DB 261 --QATNPSPAETLPSNMANQMPYSGVPPQGSNRADAIPIGYGAGRTVPQPPQMKSS 318
QY 683 VPPVSGMTAPYDSSRIWRPMPYQRDIIIRNSNLPMDVMHSSVYQTSIRERYNSLDGY 742
DB 319 FPAPPGEMVGP-----TGSLLPALPPSSA-----YMMYDGE 349
QY 743 YSVACQPPSEPR-----TTVPLPREPCGHLKTSCEQIRRKPD--QMAQYHTQKAPL 792
DB 350 GGRSHHPQPPPHAPQPGYPTTSASLONPPQH-----NLMTANPQSQFVRNHPNELI 403
QY 793 VSSITLVATQSTPPSPPLFSVDPRADFSSVSGTKFE-----DHLSHYSP--- 838
DB 404 -----EKLVMGFRGDHVASVI-QRMESGQAVDFNSVLDRLSSVGPQRG 447
QY 839 -WS 840
DB 448 GWS 450

RESULT 11
US-10-953-349-13467
; Sequence 13467, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13467
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13467

Query Match          2.6%; Score 158.5; DB 6; Length 456;
Best Local Similarity 21.5%; Pred. No. 0.057;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTRTFPLNKVGVNNVTYTTAGNVISVIGSTETTGKIVPST 493

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Db 740 RYKELEEQIQESAREAREMERALLQGERAREBRALLQKEQKAVDQ-----LQEKVLALET 792

Qy 1038 GELQSDYTEDA---TDYKPDRIE---LELSALDTEPD-----QOSEPIEE--- 1078

Db 793 G-IQERDKEALAELETETKLFEDLEFQQLERESRVEEERELAQGGLLRSAKELLSIAKAR 851

Qy 1079 -----ILDIQIG-ISSQNDOLNGMAVENGHVQOQKKEPK 1114

Db 852 KERLAILDSQAGQIRAOAVQESERILARDKNASLIQLQKEKEK 893

RESULT 14

US-11-293-697-4492

/ Sequence 4492, Application US/11293697

/ Publication No. US20060105376A1

/ GENERAL INFORMATION:

/ APPLICANT: HELIX RESEARCH INSTITUTE

/ TITLE OF INVENTION: Novel full length cDNA

/ FILE REFERENCE: H1-A0106

/ CURRENT APPLICATION NUMBER: US/11/293,697

/ CURRENT FILING DATE: 2005-12-05

/ PRIOR APPLICATION NUMBER: US/10/108,260

/ PRIOR FILING DATE: 2002-03-28

/ NUMBER OF SEQ ID NOS: 5458

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 4492

/ LENGTH: 950

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-293-697-4492

Query Match 2.4%; Score 152; DB 7; Length 950;

Best Local Similarity 19.9%; Pred. No. 0.35;

Matches 178; Conservative 114; Mismatches 337; Indels 266; Gaps 44;

Qy 42 LNKLRKACRPD-----QTAINIDIDLVPNFPALLOLVGQVPHQSIKLSNIGE--- 91

Db 109 VVKLQKQALDLELOMEKQKQETAGKQKTKDLOIADLSL-DSKDPHSHMKAKQKSGKEQ 167

Qy 92 ---NKHYE-----VAKKCEDLALYLKPLSGKGVASINQASLRPMQ----- 131

Db 168 LDIMKKQYQLESRLDEILSRIAKE-TEEIKDLEBQLTGQIAAN---BALKKDLGAVIS 223

Qy 132 --RKVLTVNCOVVEEGEVNRRAMRAARSIGERTVTELLIQHQNPQOLSNLMAAVPARGC 189

Db 224 GLQEVLTGKQATQAKQNECRKLRDEKETLLQRLTEV---EGERDLRLS----- 269

Qy 190 QPLGPMQDEALKVLVLAEDGALSRLVLVFFVQRLRPRRPAASKTSIGHVVOULTYRA 249

Db 270 ---VAMDAENRKELAELE--SALOEO-----HEVNASLQQTQDGLSAYEAELEARL 316

Qy 250 SCFKVTKRDEDSLMQLKEEFSRYEALRR-----EHDQIVHIAM-ENGRLISPE 298

Db 317 NL-----RDMAEQKLEKELKVTRLTQLBQSALQAELEKERRQALKNMLGKAQSEEEK 369

Qy 299 QWSSLLYGDLAH-----KSHMOSITDKLOSPESSFAKSVQELTIVIQ-RTG 342

Db 370 QENSELHAQLKLODDNNLLKQQLKDFQNLHNVVDGLVRPEVAVARVDELRRKLLGLTG 429

Qy 343 D-----PAIL-----NRLRPHLELLANTDPRNDVASFWEQLENM--VAKVTVNHGLVD 390

Db 430 ENNIHSPSDVLQKSLADLOKQFSEILARSKWERDEAQRERKLQDEMALQDEKGLATGQE 489

Qy 391 FIO-----NYSRKGHETP-----OPQPNKYKT 413

Db 490 FQACERALEARNMFKRQHEARIQOMENEHYLOENLKSMBEIQGLTLOLQGEADEEKE 549

Qy 414 SKCRDLRQGGCGPRGNTCTFAHQEE--LEKYRLNKKINATVTRFFPLANKYGVANNVT 470

Db 550 RLIAQLRE---LEKKKLEDAKSQEQVFGIDKELKKLKAIVATSDKLATAEILLTIAQDK 606

Qy 471 TTAGNVISV-----IGSTET-TGKIVPSTNGISNAENSVS--QLISRSTDTSLALET 520

Db 607 SLHGTVMKINGRARELEQEAERFRRKAAQARDLTPRAEIELLOVLNRQKGBQRF-LEW 665

Qy 521 VKKGVKANGONMAAPSADSVTENK-----IGSPKTPVSNVAATSG-PS 566

Db 666 EKTGVGTGANSQVLBEIEKINETMERQRTIELARLOVLDLTGSDNKGFPENVLBEIELR 725

Qy 567 NVGTELNSVPOKSSPFLTRVVPY---PPHSENIQVFQDPRTO-----IPREVP- 611

Db 726 EVSYQNDYISSMADDPKRGKGYWFMPPPSSKVSSSHSSQATQDGVGLKYASTVPRKPR 785

Qy 612 ---QYFQTSYPPRPPT-----VPAGVAPCVP-RFVRG--NNVPSSY-----P 648

Db 786 PGQDQKSGSQPPRPAAGVWVYSPIRSGHLKLFPSNRADCGSGQSESELDDQEPFPVP 845

Qy 649 PASMYPADHYSTFSPDRKNSSP-----YQPPPPQ-----YGVPPVPSC 689

Db 846 PGYMWY-----TVLP---DGSPPVQGMALVAPRPLPNNSSPRLTGTIVVYGPFPAGAP 896

Qy 690 MYAPVYDSRIRMRPMPYQRDILIRNSLP--PMDVHSSV---YQTSLERYNSL 739

Db 897 VYGP-----PPPVF-----STFPIPGVLHCNVPEHHNLVSGKTYNSL 934

RESULT 15

US-10-953-349-21437

/ Sequence 21437, Application US/10953349

/ Publication No. US20060107345A1

/ GENERAL INFORMATION:

/ APPLICANT: ALEXANDROV, Nikolai et al.

/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

/ FILE REFERENCE: 2750-1579PUS2

/ CURRENT APPLICATION NUMBER: US/10/953,349

/ CURRENT FILING DATE: 2004-09-30

/ NUMBER OF SEQ ID NOS: 40252

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 21437

/ LENGTH: 343

/ TYPE: PRT

/ ORGANISM: Glycine max

US-10-953-349-21437

Query Match 2.4%; Score 151; DB 6; Length 343;

Best Local Similarity 23.6%; Pred. No. 0.099; Mismatches 131; Indels 118; Gaps 19;

Matches 87; Conservative 32;

Qy 535 AGPSADSVTENKIGSP-----PKTPVSNVAATSGAPSN--VGTELNSVPOKSSPFLT 584

Db 31 AARPSAQMAASNTQAPQCPRYIIPTRPMN-SALRQHPQNOYLRPSDQYRTQLVAPQPI 89

Qy 585 RVVPYR-PHSENIQVFQDPRTOIPREVPQYFQYGY-----YPPR-----PTVPAGVA 630

Db 90 PEOVTSPRPVQFHSYHQPOQQ--QQPQQQQQQMSQOVQPEQPPMQSVBPSBNVYP 147

Qy 631 PCVPRFVSNNTPESSLPASMPYADHYSTFPR--DRKNSSPY-----OPPP 677

Db 148 PYQPN--QATNPSPELTLPNSMAQMPYSGVPPQGSNRDALPYGVGAGRTVPQPPQ 205

Qy 678 QYGVPRVPSGMVAPVYDSRIRMRPMPYQRDILIRNSGLPMDVHSSVYQTSLERYN 737

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Qy 738 SLDGYSVAQCPSPSR-----TVVLPREPCGHLKTSCEBQIRKRPD--QMAQYHT 787

Db 237 MYDGEGRSHNRPQRPNFAQPGYRPTSASLQNPQGH-----NLMTVRNPNOSQFVRNRP 290

Qy 788 QKAPLVSTLRYALQSPRPSPFLGVDFRADPSGSVSGTKPRP-----DHLSHY 836

Db 291 YNELI-----EKLVSNGFRGDHVASVT-QRMBSGQADVNSVLDRLSSV 334

Qy 837 SP-----WS 840

Db 335 GPQRGWS 342

Wed May 31 11:47:35 2006

us-10-619-992-2.rapbn

Page 10

Search completed: May 24, 2006, 12:53:48
Job time : 15 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:48:59 ; Search time 299 Seconds
(without alignments)
6082.290 Million cell updates/sec

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Perfect score: 6215
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pending Patents AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6215	100.0	1191	US-10-170-205E-31443	Sequence 31443, A
2	6215	100.0	1191	US-10-619-992-2	Sequence 2, Appl1
3	6215	100.0	1191	US-60-452-680-22109	Sequence 22109, A
4	6215	100.0	1191	US-60-453-050-13599	Sequence 13599, A
5	6215	100.0	1191	US-60-453-135-13599	Sequence 13599, A
6	6215	100.0	1191	US-60-466-412-13599	Sequence 13599, A
7	6207	99.9	1191	US-10-619-992-4	Sequence 4, Appl1
8	5880	94.6	1137	US-60-243-734-16	Sequence 16, Appl1
9	5525	88.9	1062	US-10-170-205E-29971	Sequence 29971, A
10	5525	88.9	1062	US-60-452-680-22108	Sequence 22108, A
11	5525	88.9	1062	US-60-453-050-13598	Sequence 13598, A
12	5525	88.9	1062	US-60-453-135-13598	Sequence 13598, A
13	5525	88.9	1062	US-60-466-412-13598	Sequence 13598, A
14	5463	88.2	1048	US-10-485-225-8	Sequence 8, Appl1
15	4416	71.1	869	US-09-488-725A-3499	Sequence 3499, Ap
16	4416	71.1	869	US-10-258-898A-3499	Sequence 3499, Ap
17	4416	71.1	869	US-10-286-897-3499	Sequence 3499, Ap
18	4066.5	65.4	812	US-09-488-725A-3500	Sequence 3500, Ap
19	4066.5	65.4	812	US-10-258-898A-3500	Sequence 3500, Ap
20	4066.5	65.4	812	US-10-286-897-3500	Sequence 3500, Ap
21	2685	43.2	1134	US-60-710-726-114	Sequence 114, App1
22	2685	43.2	1134	US-60-733-162-682	Sequence 682, App
23	2681.5	43.1	1133	US-10-170-205E-7090	Sequence 7090, Ap
24	2665.5	42.9	1132	US-10-461-673-10443	Sequence 10443, A
25	2665	42.9	1132	US-60-452-680-20520	Sequence 20520, A
26	2665	42.9	1132	PCT-US00-30653-280	Sequence 280, App1
27	2106	33.9	421	US-60-243-734-15	Sequence 15, Appl1
28	1712.5	27.6	628	US-60-262-095-6	Sequence 6, Appl1
29	1712.5	27.6	628	US-09-488-725A-7071	Sequence 7071, Ap
30	1593	25.6	306	US-10-258-898A-7072	Sequence 7072, Ap
31	1593	25.6	306	US-10-286-897-7072	Sequence 7072, Ap
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41	1593	25.6	306	US-10-286-897-7071	Sequence 7071, Ap
42	1593	25.6	306	US-10-286-897-7071	Sequence 7071, Ap
43	1593	25.6	306	US-10-286-897-7071	Sequence 7071, Ap
44	1492.5	24.0	296	US-60-191-681-19706	Sequence 19706, A
45	886	14.3	27	PCT-US00-30653-281	Sequence 281, App
				US-09-758-461-704	Sequence 704, App

ALIGNMENTS

RESULT 1
US-10-170-205E-31443
; Sequence 31443, Application US/10170205E
; GENERAL INFORMATION:

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; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31443
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-170-205E-31443

Query Match      100.0%; Score 6215; DB 31; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 MAAVNARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVVOQLERFPQASTSIG 240
QY 241 HVOVLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIVHIAEAGLRISPQW 300
DB 241 HVOVLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIVHIAEAGLRISPQW 300
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QY 1081 DIQIGISSONDQLNGMAVENGHVQOHQKEPPKOKKOSLGEDHYILEEQKTIILPVTSCF 1140
DB 1081 DIQIGISSONDQLNGMAVENGHVQOHQKEPPKOKKOSLGEDHYILEEQKTIILPVTSCF 1140
QY 1141 SQPLPVSTISNASCLEPITTSVSAGNLLKTHVSEDKNDFLKPVANGKWN 1191
DB 1141 SQPLPVSTISNASCLEPITTSVSAGNLLKTHVSEDKNDFLKPVANGKWN 1191

RESULT 2
US-10-619-992-2
; Sequence 2, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefenelder, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-619-992-2

Query Match      100.0%; Score 6215; DB 36; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVOAAQWTEFLSCPICTVNEFDENVHKPISLGCSTHTVCTCTKLNKLRKACPFDDQTAINTD 60
DB 1 MPVOAAQWTEFLSCPICTVNEFDENVHKPISLGCSTHTVCTCTKLNKLRKACPFDDQTAINTD 60
QY 61 IDVLVFNFAILLQVGAQVDPDHOSIKLSNUGENKHYEVAKKCYEDIALYIKPLSGKGVAS 120
DB 61 IDVLVFNFAILLQVGAQVDPDHOSIKLSNUGENKHYEVAKKCYEDIALYIKPLSGKGVAS 120
QY 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLISANL 180
DB 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLISANL 180
QY 181 MAAVNARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVVOQLERFPQASTSIG 240
DB 181 MAAVNARCGOFLGPAMQEBALKVLVLLALDGSALSRKVLVLFVVOQLERFPQASTSIG 240
QY 241 HVOVLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIVHIAEAGLRISPQW 300
DB 241 HVOVLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIVHIAEAGLRISPQW 300
QY 301 SSLVGLDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELLANI 360

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Db 301 SLLIGDLAHKSHMOSIIDKLOSPESFASVOELTIVLORTGDPALNLRPHLELLANI 360
Qy 361 DPNPAVSPTEQLEENAMVAVKTVHGLVDFIQNSRKHEPTPOPOPNKYKTSMCRDLR 420
Db 361 DPNPAVSPTEQLEENAMVAVKTVHGLVDFIQNSRKHEPTPOPOPNKYKTSMCRDLR 420
Qy 421 OQGGCPRGNTCTFAHGOEELKRYLRNKKINATVTRFPLNKGUNNTYTTTANISVI 480
Db 421 OQGGCPRGNTCTFAHGOEELKRYLRNKKINATVTRFPLNKGUNNTYTTTANISVI 480
Qy 481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLALETVKVKGVGANGONAAAPSAD 540
Db 481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLALETVKVKGVGANGONAAAPSAD 540
Qy 541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Db 541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Qy 601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
Db 601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
Qy 661 FSPRDMNSPYOPPEPOYPGPVPPVSGMYAPVYDSRRIWPRPMYQORDIIRSNLPPM 720
Db 661 FSPRDMNSPYOPPEPOYPGPVPPVSGMYAPVYDSRRIWPRPMYQORDIIRSNLPPM 720
Qy 721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIIRKRD 780
Db 721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIIRKRD 780
Qy 781 QMAQYHTQAKPLVSSSTLPAVATOSPPTPSPPLFSYVDFRADSESYSGTKFEEDHLSHSPWS 840
Db 781 QMAQYHTQAKPLVSSSTLPAVATOSPPTPSPPLFSYVDFRADSESYSGTKFEEDHLSHSPWS 840
Qy 841 CGTIGSCINAIIDSEPDVANSNAVLMDDSGDKRVHLFETORTKXEDPIIPSDGP 900
Db 841 CGTIGSCINAIIDSEPDVANSNAVLMDDSGDKRVHLFETORTKXEDPIIPSDGP 900
Qy 901 IISKWGISRSRSTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGENATS 960
Db 901 IISKWGISRSRSTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGENATS 960
Qy 961 SAHYVERDFIYTDLSGHRKHSSTGDLLELOQAKSNLLOREANALAMQKNMSLDE 1020
Db 961 SAHYVERDFIYTDLSGHRKHSSTGDLLELOQAKSNLLOREANALAMQKNMSLDE 1020
Qy 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDKPRDIIELELSALDDEPDGSEPIEEL 1080
Db 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDKPRDIIELELSALDDEPDGSEPIEEL 1080
Qy 1081 DIOLGISSQNDOLLNGMAVENGHVQOHQKEPKQKQSLGEBDHVILEBOKITLPTVSGF 1140
Db 1081 DIOLGISSQNDOLLNGMAVENGHVQOHQKEPKQKQSLGEBDHVILEBOKITLPTVSGF 1140
Qy 1141 SQPLPVISINASCPIITTSVSAGNLLKTRHVSSEKNDPLKPYANGKMNVS 1191
Db 1141 SQPLPVISINASCPIITTSVSAGNLLKTRHVSSEKNDPLKPYANGKMNVS 1191

; SEQ ID NO 22109
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22109
Query Match 100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0; Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFVQAQWTEFLSCPIYNEPDENVHKKPISLCSHTVCTCLNKRKACPPDOTAINTD 60
Db 1 MFVQAQWTEFLSCPIYNEPDENVHKKPISLCSHTVCTCLNKRKACPPDOTAINTD 60
Qy 61 IDVLVFNFALLQVGAQVDPHQSIKLSNIDENKHEVAKCYEDLALYIKPISGGGVAS 120
Db 61 IDVLVFNFALLQVGAQVDPHQSIKLSNIDENKHEVAKCYEDLALYIKPISGGGVAS 120
Qy 121 LMQSALSRPMOKRLTVLNCOLVEEGRVAMRAARSLGERTYTELILQHPQOLSANL 180
Db 121 LMQSALSRPMOKRLTVLNCOLVEEGRVAMRAARSLGERTYTELILQHPQOLSANL 180
Qy 181 MAAYBARCGCFIPAMOEALKLVLLALEDSGALSRLKVLVLFVQGRLEBRFPQASTSIG 240
Db 181 MAAYBARCGCFIPAMOEALKLVLLALEDSGALSRLKVLVLFVQGRLEBRFPQASTSIG 240
Qy 241 HVVQLLYRASCFKVTYKDESSLMOLEEFNRYEALRREHDAQIYHIADEAGLRISPEQ 300
Db 241 HVVQLLYRASCFKVTYKDESSLMOLEEFNRYEALRREHDAQIYHIADEAGLRISPEQ 300
Qy 301 SLLIGDLAHKSHMOSIIDKLOSPESFASVOELTIVLORTGDPALNLRPHLELLANI 360
Db 301 SLLIGDLAHKSHMOSIIDKLOSPESFASVOELTIVLORTGDPALNLRPHLELLANI 360
Qy 361 DPNPAVSPTEQLEENAMVAVKTVHGLVDFIQNSRKHEPTPOPOPNKYKTSMCRDLR 420
Db 361 DPNPAVSPTEQLEENAMVAVKTVHGLVDFIQNSRKHEPTPOPOPNKYKTSMCRDLR 420
Qy 421 OQGGCPRGNTCTFAHGOEELKRYLRNKKINATVTRFPLNKGUNNTYTTTANISVI 480
Db 421 OQGGCPRGNTCTFAHGOEELKRYLRNKKINATVTRFPLNKGUNNTYTTTANISVI 480
Qy 481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLALETVKVKGVGANGONAAAPSAD 540
Db 481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLALETVKVKGVGANGONAAAPSAD 540
Qy 541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Db 541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Qy 601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
Db 601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
Qy 661 FSPRDMNSPYOPPEPOYPGPVPPVSGMYAPVYDSRRIWPRPMYQORDIIRSNLPPM 720
Db 661 FSPRDMNSPYOPPEPOYPGPVPPVSGMYAPVYDSRRIWPRPMYQORDIIRSNLPPM 720
Qy 721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIIRKRD 780
Db 721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIIRKRD 780
Qy 781 QMAQYHTQAKPLVSSSTLPAVATOSPPTPSPPLFSYVDFRADSESYSGTKFEEDHLSHSPWS 840
Db 781 QMAQYHTQAKPLVSSSTLPAVATOSPPTPSPPLFSYVDFRADSESYSGTKFEEDHLSHSPWS 840
Qy 841 CGTIGSCINAIIDSEPDVANSNAVLMDDSGDKRVHLFETORTKXEDPIIPSDGP 900
Db 841 CGTIGSCINAIIDSEPDVANSNAVLMDDSGDKRVHLFETORTKXEDPIIPSDGP 900
Qy 901 IISKWGISRSRSTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGENATS 960
Db 901 IISKWGISRSRSTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGENATS 960

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QY 961 SAHYERDRFIVTDLSGHRKHSSTGDLISLEIQAKSNLLQREANALAMQOKNMSLDE 1020
Db 961 SAHYERDRFIVTDLSGHRKHSSTGDLISLEIQAKSNLLQREANALAMQOKNMSLDE 1020
QY 1021 GRHLTLNLISKEIEIRNGELQSDYEDATDTKPRDRIEIELSALDTPDEPDGQSEPIEIL 1080
Db 1021 GRHLTLNLISKEIEIRNGELQSDYEDATDTKPRDRIEIELSALDTPDEPDGQSEPIEIL 1080
QY 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBQKTLIPVTSCE 1140
Db 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBQKTLIPVTSCE 1140
QY 1141 SGPPLVVISISNASCCLPITTSVSAGNLIKTHVMSSEKNDPLKPVANGKWN 1191
Db 1141 SGPPLVVISISNASCCLPITTSVSAGNLIKTHVMSSEKNDPLKPVANGKWN 1191

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RESULT 4
US-60-453-050-13599
; Sequence 13599, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453, 050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13599

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Query Match 100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPVQAAQWTEFLSCPICYNEFDENVHAKPISLGCSTHTVCKTCLNKLHAKCAPFDQTAINTD 60
Db 1 MPVQAAQWTEFLSCPICYNEFDENVHAKPISLGCSTHTVCKTCLNKLHAKCAPFDQTAINTD 60
QY 61 IDVLPNVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
Db 61 IDVLPNVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
QY 121 LNSQALSRRMOKRLVTLVNCQVVEEGRVAMPARASLGERVTTELLOHONPOQLSANL 180
Db 121 LNSQALSRRMOKRLVTLVNCQVVEEGRVAMPARASLGERVTTELLOHONPOQLSANL 180
QY 181 MAAVRARGCQFLGAPAMQEBALKVLIALDEGSLSRKVLVLFVQRLERPPPOASTSTIG 240
Db 181 MAAVRARGCQFLGAPAMQEBALKVLIALDEGSLSRKVLVLFVQRLERPPPOASTSTIG 240
QY 241 HAVVQLLYRASCFKVTTRDDSSIMOLKEEFRSYEALRRHDQIVIAIEAGLRISPEQM 300
Db 241 HAVVQLLYRASCFKVTTRDDSSIMOLKEEFRSYEALRRHDQIVIAIEAGLRISPEQM 300
QY 301 SELLVYDLDLHKSHMOSIIDKLOSPEFAKVOELTIVLORTGDPANILRLPHLELIANI 360
Db 301 SELLVYDLDLHKSHMOSIIDKLOSPEFAKVOELTIVLORTGDPANILRLPHLELIANI 360
QY 361 DPNPDVSPTEWQLEENAMVAVKTVTHGLVDFIQNSRKGHETPOPONSKYKTSKCRDLR 420
Db 361 DPNPDVSPTEWQLEENAMVAVKTVTHGLVDFIQNSRKGHETPOPONSKYKTSKCRDLR 420
QY 421 OGGGCGRGNTCTPAHSHOELEKRLNKKINATVTFPLNKGUNNTYTTTGANIVSYI 480
Db 421 OGGGCGRGNTCTPAHSHOELEKRLNKKINATVTFPLNKGUNNTYTTTGANIVSYI 480

```

```

QY 481 GSTETTGKIVSTNGISNAENSVSOLISRSSTDSTLRALETVKVKGANGAAGPSAD 540
Db 481 GSTETTGKIVSTNGISNAENSVSOLISRSSTDSTLRALETVKVKGANGAAGPSAD 540
QY 541 SYTENKIGSPKTPVSNVAISAGPSNVGTLEANSIPQKSSPLTRVPVYPHSENIQYRQ 600
Db 541 SYTENKIGSPKTPVSNVAISAGPSNVGTLEANSIPQKSSPLTRVPVYPHSENIQYRQ 600
QY 601 DPTQIPPEVPQYPTQYGYPPPEPTVAGVAPCVPRFVSNVNESSLPASAPYADHYST 660
Db 601 DPTQIPPEVPQYPTQYGYPPPEPTVAGVAPCVPRFVSNVNESSLPASAPYADHYST 660
QY 661 FSPDRMNSSPYQPPPPQYGPVPPVPGMYAPVYDSRRIRWPPMYQRDDIIRNSLPPM 720
Db 661 FSPDRMNSSPYQPPPPQYGPVPPVPGMYAPVYDSRRIRWPPMYQRDDIIRNSLPPM 720
QY 721 DYMSSVYQTSIREXNYSIDGYSAVACQPPSPRTTVPRLPRPCGLKTSCEQIRKRPD 780
Db 721 DYMSSVYQTSIREXNYSIDGYSAVACQPPSPRTTVPRLPRPCGLKTSCEQIRKRPD 780
QY 781 QMAOYHTOKAPLVSSTLPVATOSPFPSPPLFVDPFRADPSESVSQTKFEEDHLSHYS 840
Db 781 QMAOYHTOKAPLVSSTLPVATOSPFPSPPLFVDPFRADPSESVSQTKFEEDHLSHYS 840
QY 841 CGTIGSCINAIIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEDPIIPPSDGP 900
Db 841 CGTIGSCINAIIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEDPIIPPSDGP 900
QY 901 IISKGAISRSSRTGYHTTDPVQATASQSAKPIISVSYVYVNAVDSRMSYNGEARS 960
Db 901 IISKGAISRSSRTGYHTTDPVQATASQSAKPIISVSYVYVNAVDSRMSYNGEARS 960
QY 961 SAHYERDRFIVTDLSGHRKHSSTGDLISLEIQAKSNLLQREANALAMQOKNMSLDE 1020
Db 961 SAHYERDRFIVTDLSGHRKHSSTGDLISLEIQAKSNLLQREANALAMQOKNMSLDE 1020
QY 1021 GRHLTLNLISKEIEIRNGELQSDYEDATDTKPRDRIEIELSALDTPDEPDGQSEPIEIL 1080
Db 1021 GRHLTLNLISKEIEIRNGELQSDYEDATDTKPRDRIEIELSALDTPDEPDGQSEPIEIL 1080
QY 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBQKTLIPVTSCE 1140
Db 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBQKTLIPVTSCE 1140
QY 1141 SGPPLVVISISNASCCLPITTSVSAGNLIKTHVMSSEKNDPLKPVANGKWN 1191
Db 1141 SGPPLVVISISNASCCLPITTSVSAGNLIKTHVMSSEKNDPLKPVANGKWN 1191

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RESULT 5
US-60-453-135-13599
; Sequence 13599, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453, 135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13599

```

```

Query Match 100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MPVQAAQWTEFLSCPICYNEFDENVHAKPISLGCSTHTVCKTCLNKLHAKCAPFDQTAINTD 60

```

Db      1 MPVQAAQWTEFLSCPICYNEFDENVKPISLGSHTVCTCLNKRKACPFQDTAINTD 60
Qy      61 IDVLPVNFALLQJVGQVDPDHOSIKLSNIGENKHYEAVAKKVEDLALYLKPLSGKGVAS 120
Db      61 IDVLPVNFALLQJVGQVDPDHOSIKLSNIGENKHYEAVAKKVEDLALYLKPLSGKGVAS 120
Qy      121 LMQSALSRRMOKRLVTLVNCQVLEEGRVRAARAASLGERVTYTELLIHOHNPQOLSANL 180
Db      121 LMQSALSRRMOKRLVTLVNCQVLEEGRVRAARAASLGERVTYTELLIHOHNPQOLSANL 180
Qy      181 MAABARAGCOFLGPAMOEALKVLALLADGALSRSKVLVLFVQBLEPFPQASTSIG 240
Db      181 MAABARAGCOFLGPAMOEALKVLALLADGALSRSKVLVLFVQBLEPFPQASTSIG 240
Qy      241 HVVOLLYRASCFKVTGRDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQM 300
Db      241 HVVOLLYRASCFKVTGRDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQM 300
Qy      301 SLLYGDLLAHKSHMOSIIDKLOSPEFPAKSVOELTIVLQRTGDPANLRLRPHLELLANI 360
Db      301 SLLYGDLLAHKSHMOSIIDKLOSPEFPAKSVOELTIVLQRTGDPANLRLRPHLELLANI 360
Qy      361 DNPDAVSPPTMQLBNAMAVAKTVVHGLVDFIONYSRKGHETFPQOPNSKYKTSKMRDLR 420
Db      361 DNPDAVSPPTMQLBNAMAVAKTVVHGLVDFIONYSRKGHETFPQOPNSKYKTSKMRDLR 420
Qy      421 OGGGCGRGNTCTFAHGOELEKYLANKKINATVTRFPLLNKGVANNVTTTGANVYSVI 480
Db      421 OGGGCGRGNTCTFAHGOELEKYLANKKINATVTRFPLLNKGVANNVTTTGANVYSVI 480
Qy      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALFTVKKVGVANGVANGONAAAPSAD 540
Db      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALFTVKKVGVANGVANGONAAAPSAD 540
Qy      541 SVTENKIGSPKTPVSNVAATSAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Db      541 SVTENKIGSPKTPVSNVAATSAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Qy      601 DPTQIPEFVPOYPQYGYPPPTPVAGVAPCVPRFVRSNVPESSLPPASMPYADHYST 660
Db      601 DPTQIPEFVPOYPQYGYPPPTPVAGVAPCVPRFVRSNVPESSLPPASMPYADHYST 660
Qy      661 FSPRDRMNSPYQPPQYGYPPVPSGMAYAVYDSRIWRPMTYQORDDIRNSLPPM 720
Db      661 FSPRDRMNSPYQPPQYGYPPVPSGMAYAVYDSRIWRPMTYQORDDIRNSLPPM 720
Qy      721 DVMHSSVYQTSLRERNSLDGYYSVACOPSPSEPTTVPLPRPCGHLKTSCEQIRKXD 780
Db      721 DVMHSSVYQTSLRERNSLDGYYSVACOPSPSEPTTVPLPRPCGHLKTSCEQIRKXD 780
Qy      781 QMAQYHTQKAPLVSTLPAVATOSPPTSPFLFVDFRADSESVSGTKFEDHLSHSPMS 840
Db      781 QMAQYHTQKAPLVSTLPAVATOSPPTSPFLFVDFRADSESVSGTKFEDHLSHSPMS 840
Qy      841 CGTIGSCINAIDSEPKDVIANSNAVIMLIDSGDVKRVHLFETORTKEEDPIIPSDGP 900
Db      841 CGTIGSCINAIDSEPKDVIANSNAVIMLIDSGDVKRVHLFETORTKEEDPIIPSDGP 900
Qy      901 IISKKGALSRSSRTGHTTDPVOATASQSAATKPIVSVDYVPVYVNAVDRMSVYGEATS 960
Db      901 IISKKGALSRSSRTGHTTDPVOATASQSAATKPIVSVDYVPVYVNAVDRMSVYGEATS 960
Qy      961 SAHYVERDRFIVYDLSGHRKHSITGDLISLELOQAKSNLILQREANALAMQKMSLDE 1020
Db      961 SAHYVERDRFIVYDLSGHRKHSITGDLISLELOQAKSNLILQREANALAMQKMSLDE 1020
Qy      1021 GHHLTNLISKEIELANGELOSYTFDADPTKPDRIEHLMLDTPDEPGOSEPIEELL 1080
Db      1021 GHHLTNLISKEIELANGELOSYTFDADPTKPDRIEHLMLDTPDEPGOSEPIEELL 1080
Qy      1081 DIOLGISSONDOLINMAVENGHFVQOHKEPPKQKOSLGEDHVLIEQKTLIPTVSCF 1140

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Db      1081 DIOLGISSONDOLINMAVENGHFVQOHKEPPKQKOSLGEDHVLIEQKTLIPTVSCF 1140
Qy      1141 SGPPLVVISNASCLPITTSVSAAGNLILKTAHVNSEKNDPLKPYANGKMNVS 1191
Db      1141 SGPPLVVISNASCLPITTSVSAAGNLILKTAHVNSEKNDPLKPYANGKMNVS 1191

RESULT 6
US-60-466-412-13599
; Sequence 13599, Application us/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FASTSEQ for windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PR1
; ORGANISM: Homo sapiens
US-60-466-412-13599

Query Match      100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MPVQAAQWTEFLSCPICYNEFDENVKPISLGSHTVCTCLNKRKACPFQDTAINTD 60
Db      1 MPVQAAQWTEFLSCPICYNEFDENVKPISLGSHTVCTCLNKRKACPFQDTAINTD 60
Qy      61 IDVLPVNFALLQJVGQVDPDHOSIKLSNIGENKHYEAVAKKVEDLALYLKPLSGKGVAS 120
Db      61 IDVLPVNFALLQJVGQVDPDHOSIKLSNIGENKHYEAVAKKVEDLALYLKPLSGKGVAS 120
Qy      121 LMQSALSRRMOKRLVTLVNCQVLEEGRVRAARAASLGERVTYTELLIHOHNPQOLSANL 180
Db      121 LMQSALSRRMOKRLVTLVNCQVLEEGRVRAARAASLGERVTYTELLIHOHNPQOLSANL 180
Qy      181 MAABARAGCOFLGPAMOEALKVLALLADGALSRSKVLVLFVQBLEPFPQASTSIG 240
Db      181 MAABARAGCOFLGPAMOEALKVLALLADGALSRSKVLVLFVQBLEPFPQASTSIG 240
Qy      241 HVVOLLYRASCFKVTGRDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQM 300
Db      241 HVVOLLYRASCFKVTGRDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQM 300
Qy      301 SLLYGDLLAHKSHMOSIIDKLOSPEFPAKSVOELTIVLQRTGDPANLRLRPHLELLANI 360
Db      301 SLLYGDLLAHKSHMOSIIDKLOSPEFPAKSVOELTIVLQRTGDPANLRLRPHLELLANI 360
Qy      361 DNPDAVSPPTMQLBNAMAVAKTVVHGLVDFIONYSRKGHETFPQOPNSKYKTSKMRDLR 420
Db      361 DNPDAVSPPTMQLBNAMAVAKTVVHGLVDFIONYSRKGHETFPQOPNSKYKTSKMRDLR 420
Qy      421 OGGGCGRGNTCTFAHGOELEKYLANKKINATVTRFPLLNKGVANNVTTTGANVYSVI 480
Db      421 OGGGCGRGNTCTFAHGOELEKYLANKKINATVTRFPLLNKGVANNVTTTGANVYSVI 480
Qy      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALFTVKKVGVANGVANGONAAAPSAD 540
Db      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALFTVKKVGVANGVANGONAAAPSAD 540
Qy      541 SVTENKIGSPKTPVSNVAATSAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Db      541 SVTENKIGSPKTPVSNVAATSAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Qy      601 DPTQIPEFVPOYPQYGYPPPTPVAGVAPCVPRFVRSNVPESSLPPASMPYADHYST 660
Db      601 DPTQIPEFVPOYPQYGYPPPTPVAGVAPCVPRFVRSNVPESSLPPASMPYADHYST 660

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QY 661 FSPDRMNSPYQPPPOGYGVPVPVSGMYA PVDYSRIIMRPMPYQORDIIRNSL.PPM 720
| | | | |
Db 661 FSPDRMNSPYQPPPOGYGVPVPVSGMYA PVDYSRIIMRPMPYQORDIIRNSL.PPM 720
QY 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPSSEPRITVPLPREPCGHLKLTSCBQIRKRD 780
| | | | |
Db 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPSSEPRITVPLPREPCGHLKLTSCBQIRKRD 780
QY 761 QMAQYHTQKAPLVSSSTLPVATQSPPTPSPLFSVDPRADSESVSGTKFEEDHLSHYSPWS 840
| | | | |
Db 761 QMAQYHTQKAPLVSSSTLPVATQSPPTPSPLFSVDPRADSESVSGTKFEEDHLSHYSPWS 840
QY 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDSDGVKRRVHLFETQRTKEEDPIIPSDGP 900
| | | | |
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDSDGVKRRVHLFETQRTKEEDPIIPSDGP 900
QY 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
| | | | |
Db 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
QY 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQAANSLLLOREANALAMQKXNSLDE 1020
| | | | |
Db 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQAANSLLLOREANALAMQKXNSLDE 1020
QY 1021 GRLTLNLISKEIELRNGELQSDYTEDATDTKPRDIELELSALDDEPDGQSEPIEELL 1080
| | | | |
Db 1021 GRLTLNLISKEIELRNGELQSDYTEDATDTKPRDIELELSALDDEPDGQSEPIEELL 1080
QY 1081 DIQLGISSQNDOLNMAVENGHPVQOHQKEPPKQKQSLGEDHVLLEBOKTILPVTSCF 1140
| | | | |
Db 1081 DIQLGISSQNDOLNMAVENGHPVQOHQKEPPKQKQSLGEDHVLLEBOKTILPVTSCF 1140
QY 1141 SGPPLPVISINAGCLPITTSVSAGNLLKTHWSEDKNDLFLKPVANGKMVNS 1191
| | | | |
Db 1141 SGPPLPVISINAGCLPITTSVSAGNLLKTHWSEDKNDLFLKPVANGKMVNS 1191

RESULT 7
US-10-619-992-4
; Sequence 4, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seies, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-992-4

Query Match 99.9%; Score 6207; DB 36; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPVOAAQMTBFLSCPICNNEFDENVHKPISLGCSTYVCKTCLNKLHKKACPFQOTAINND 60
| | | | |
Db 1 MAVOAAQMTBFLSCPICNNEFDENVHKPISLGCSTYVCKTCLNKLHKKACPFQOTAINND 60
QY 61 IDVLPNPFLLLOLVGQVPHQSIKLSNIGENGYEYAKKCVEDLLALYLKPLSGGKGVAS 120
| | | | |
Db 61 IDVLPNPFLLLOLVGQVPHQSIKLSNIGENGYEYAKKCVEDLLALYLKPLSGGKGVAS 120

QY 121 LNOALSRLPMQKLVTLVNCQVLEEGRVVRAMRAARSLGERTVTELLLOHNPOLSANL 180
| | | | |

Db 121 LNOALSRLPMQKLVTLVNCQVLEEGRVVRAMRAARSLGERTVTELLLOHNPOLSANL 180
| | | | |
QY 181 WAAVARBGQFLGRAMOEALKVTLALLEDGALSRLKVLVLFVQRLERFRFOASTSTIG 240
| | | | |
Db 181 WAAVARBGQFLGRAMOEALKVTLALLEDGALSRLKVLVLFVQRLERFRFOASTSTIG 240
QY 241 HVOVLLYRASCPKVKRDEBDSGLMQLKEFRSYEALRREHDAQIYHIAEAGLRISPEQM 300
| | | | |
Db 241 HVOVLLYRASCPKVKRDEBDSGLMQLKEFRSYEALRREHDAQIYHIAEAGLRISPEQM 300
QY 301 SLLLYGDLAKSHMOSIIDKLOSPESPAKSVQELTIVLQRTDPAANLRLPHLELLANI 360
| | | | |
Db 301 SLLLYGDLAKSHMOSIIDKLOSPESPAKSVQELTIVLQRTDPAANLRLPHLELLANI 360
QY 361 DPNPAVSPFTWQOLNANAVATVTVHGLVDFIONTSRKCHETPOQPNKXYTSMCRDR 420
| | | | |
Db 361 DPNPAVSPFTWQOLNANAVATVTVHGLVDFIONTSRKCHETPOQPNKXYTSMCRDR 420
QY 421 QQGGCPRGNTCTFAHSELEKYLRLNKKINATVTFPLNKKVGVNNTVTTAGNVISVI 480
| | | | |
Db 421 QQGGCPRGNTCTFAHSELEKYLRLNKKINATVTFPLNKKVGVNNTVTTAGNVISVI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSITLPALETYKVKVKGANGONAGPSAD 540
| | | | |
Db 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSITLPALETYKVKVKGANGONAGPSAD 540
QY 541 SVTENKIGSPKTPVSNVATASGPNVGTETLNSVPOKSPFLTRPVY PPHSENIQYQ 600
| | | | |
Db 541 SVTENKIGSPKTPVSNVATASGPNVGTETLNSVPOKSPFLTRPVY PPHSENIQYQ 600
QY 601 DPTQIPEFVPOYPOGTGYPPPTVPAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
| | | | |
Db 601 DPTQIPEFVPOYPOGTGYPPPTVPAGVAPCVPRFVRNNVPESLPPASMPYADHYST 660
QY 661 FSPDRMNSPYQPPPOGYGVPVPVSGMYA PVDYSRIIMRPMPYQORDIIRNSL.PPM 720
| | | | |
Db 661 FSPDRMNSPYQPPPOGYGVPVPVSGMYA PVDYSRIIMRPMPYQORDIIRNSL.PPM 720
QY 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPSSEPRITVPLPREPCGHLKLTSCBQIRKRD 780
| | | | |
Db 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPSSEPRITVPLPREPCGHLKLTSCBQIRKRD 780
QY 781 QMAQYHTQKAPLVSSSTLPVATQSPPTPSPLFSVDPRADSESVSGTKFEEDHLSHYSPWS 840
| | | | |
Db 781 QMAQYHTQKAPLVSSSTLPVATQSPPTPSPLFSVDPRADSESVSGTKFEEDHLSHYSPWS 840
QY 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDSDGVKRRVHLFETQRTKEEDPIIPSDGP 900
| | | | |
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDSDGVKRRVHLFETQRTKEEDPIIPSDGP 900
QY 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
| | | | |
Db 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
QY 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQAANSLLLOREANALAMQKXNSLDE 1020
| | | | |
Db 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQAANSLLLOREANALAMQKXNSLDE 1020
QY 1021 GRLTLNLISKEIELRNGELQSDYTEDATDTKPRDIELELSALDDEPDGQSEPIEELL 1080
| | | | |
Db 1021 GRLTLNLISKEIELRNGELQSDYTEDATDTKPRDIELELSALDDEPDGQSEPIEELL 1080
QY 1081 DIQLGISSQNDOLNMAVENGHPVQOHQKEPPKQKQSLGEDHVLLEBOKTILPVTSCF 1140
| | | | |
Db 1081 DIQLGISSQNDOLNMAVENGHPVQOHQKEPPKQKQSLGEDHVLLEBOKTILPVTSCF 1140
QY 1141 SGPPLPVISINAGCLPITTSVSAGNLLKTHWSEDKNDLFLKPVANGKMVNS 1191
| | | | |
Db 1141 SGPPLPVISINAGCLPITTSVSAGNLLKTHWSEDKNDLFLKPVANGKMVNS 1191

RESULT 8


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US-60-243-734-16
; Sequence 16, Application US/60243734
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00932
; CURRENT APPLICATION NUMBER: US/60/243, 734
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: HUMAN
US-60-243-734-16

Query Match      94.6%; Score 5880; DB 47; Length 1137;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1136; Conservative 1; Mismatches 0; Indels 54; Gaps 3;

QY      1 MPEVQAQWTEFLSCPICTYNEFDENVAHKPIISGCSHTVCKTKLHKKACPEPDQAIIND 60
DB      1 MPEVQAQWTEFLSCPICTYNEFDENVAHKPIISGCSHTVCKTKLHKKACPEPDQAIIND 60
QY      61 IDVLVFNALLQLVGAQVBDHOSIKLSNGENKHYEAVAKKCVEDIALYIKPLSGKGVAS 120
DB      61 IDVLVFNALLQLVGAQVBDHOSIKLSNGENKHYEAVAKKCVEDIALYIKPLSGKGVAS 120
QY      121 INQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLSGERVTTELIIQHNPQOLSANL 180
DB      121 INQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLSGERVTTELIIQHNPQOLSANL 180
QY      181 MAAVBARGCOFIPGPAWQEBALKVLIALLEDGALSRSKVLVLFVVOLEPRFPOASTSIG 240
DB      181 MAAVBARGCOFIPGPAWQEBALKVLIALLEDGALSRSKVLVLFVVOLEPRFPOASTSIG 240
QY      241 HVVOLLVYRASCFTVKTRDEDSIMQKEEPRSYEALREHDAQIVHIMEAGLRISPEQM 300
DB      241 HVVOLLVYRASCFTVKTRDEDSIMQKEEPRSYEALREHDAQIVHIMEAGLRISPEQM 300
QY      301 SSLLVGDLAKHKHMSIINKLOSPEFAKSVQELTIVLQRTGDPALNRLRPHLELLANI 360
DB      301 SSLLVGDLAKHKHMSIINKLOSPEFAKSVQELTIVLQRTGDPALNRLRPHLELLANI 360
QY      361 DNPPAVSPTWOLENAAVAVKTVVHGLVDFIIONYSRKGHEPRPOPONSKYKTSKCRDR 420
DB      361 DNPPAVSPTWOLENAAVAVKTVVHGLVDFIIONYSRKGHEPRPOPONSKYKTSKCRDR 420
QY      421 QGGGCGRGNTCTFAHSEBELKRYRLNKKINATVTRTFPLNKGVANNVTAGNVISVI 480
DB      421 QGGGCGRGNTCTFAHSEBELKRYRLNKKINATVTRTFPLNKGVANNVTAGNVISVI 480
QY      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALETVKVKGAVANGQAAAPSD 540
DB      481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLALETVKVKGAVANGQAAAPSD 540
QY      541 SYTENKIGSPKTPVSNVATASGSPNGTELSVPOKSSPFLTRVPVYPVPHSENIQYQ 600
DB      541 SYTENKIGSPKTPVSNVATASGSPNGTELSVPOKSSPFLTRVPVYPVPHSENIQYQ 600
QY      601 DERTQIPFEVPOYPOTGYYPPPTVPAGVAPCVPRFVRSNNVDESSLPPASMPYADHYST 660
DB      601 DERTQIPFEVPOYPOTGYYPPPTVPAGVAPCVPRFVRSNNVDESSLPPASMPYADHYST 660
QY      661 FSPRDMNSSPYOPPPQPGVPPVPSGMYAVVYSRRIWRPMYORDIIRNSNLPY 720
DB      661 FSPRDMNSSPYOPPPQPGVPPVPSGMYAVVYSRRIWRPMYORDIIRNSNLPY 720
QY      721 DVHSSVYOTSLRERNLSLGGYVVAQPPSEBRTTVPJPREBCHGLKTSCEQIRKRD 780
DB      721 DVHSSVYOTSLRERNLSLGGYVVAQPPSEBRTTVPJPREBCHGLKTSCEQIRKRD 780
QY      681 DVHSSVYOTSLRERNLSLGGYVVAQPPSEBRTTVPJPREBCHGLKTSCEQIRKRD 740
DB      681 DVHSSVYOTSLRERNLSLGGYVVAQPPSEBRTTVPJPREBCHGLKTSCEQIRKRD 740
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QY      781 QMAOYHTQKAPLVSSITLVPATOSPPTPSPPLFSDVDRADPFESVSGTKFEEDHLSHYSPWS 840
DB      741 QMAOYHTQKAPLVSSITLVPATOSPPTPSPPLFSDVDRADPFESVSGTKFEEDHLSHYSPWS 800
QY      841 CGTISGCINAIIDSEPDVIANSNAYLMDSDGDYKRVALLFETORRTKEEDPIIPSDGP 900
DB      801 CGTISGCINAIIDSEPDVIANSNAYLMDSDGDYKRVALLFETORRTKEEDPIIPSDGP 860
QY      901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGNPEATS 960
DB      861 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVNAVDSRWSSYGNPEATS 920
QY      961 SAHYERDRFITYTDLSGHAKHSTGDLSELOQAQKSNLLLORENNALAMQOKMNSLDE 1020
DB      921 SAHYE-----RKHSSTGDLSELOQAQKSNLLLORENNALAMQOKMNSLDE 968
QY      1021 GRHLTLNLTSKEIELRNGELSDYEDATDTKPRDRIDLELSALDTPDEPDGSEPIEELI 1080
DB      969 GRHLTLNLTSKEIELRNGE--SDYEDATDTKPRDRIDLELSALDTPDEPDGSEPIEELI 1026
QY      1081 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKQSLGEDHVILEBQKTIIPVTSCEP 1140
DB      1027 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKQSLGEDHVILEBQKTIIPVTSCEP 1086
QY      1141 SQPLPVYSINASCPIPTTSVSAKNILKTHVMSSEKNDLKPVANCKMNS 1191
DB      1087 SQPLPVYSINASCPIPTTSVSAKNILKTHVMSSEKNDLKPVANCKMNS 1137

RESULT 9
US-10-170-205E-29971
; Sequence 29971, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CLO01381
; CURRENT APPLICATION NUMBER: US/10/170, 209E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29971
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-29971

Query Match      88.9%; Score 5529; DB 31; Length 1062;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      130 MOKRLVTLVNCOLVEEGRVRAARAASLSGERVTTELIIQHNPQOLSANLMAAVBARGC 189
DB      1 MOKRLVTLVNCOLVEEGRVRAARAASLSGERVTTELIIQHNPQOLSANLMAAVBARGC 60
QY      190 QFLGPAWQEBALKVLIALLEDGALSRSKVLVLFVVOLEPRFPOASTSIGHYVOLLYRA 249
DB      61 QFLGPAWQEBALKVLIALLEDGALSRSKVLVLFVVOLEPRFPOASTSIGHYVOLLYRA 120
QY      250 SCFKYTKRDEDSIMQKEEPRSYEALREHDAQIVHIMEAGLRISPEOWSSLLVGDILA 309
DB      121 SCFKYTKRDEDSIMQKEEPRSYEALREHDAQIVHIMEAGLRISPEOWSSLLVGDILA 180
QY      310 HKSHMSIINKLOSPEFAKSVQELTIVLQRTGDPALNRLRPHLELLANIDNPPAVSP 369
DB      181 HKSHMSIINKLOSPEFAKSVQELTIVLQRTGDPALNRLRPHLELLANIDNPPAVSP 240
QY      370 TWEOLENAAVAVKTVVHGLVDFIIONYSRKGHETPPOPONSKYKTSKCRDLROGGCGPRGT 429
DB      241 TWEOLENAAVAVKTVVHGLVDFIIONYSRKGHETPPOPONSKYKTSKCRDLROGGCGPRGT 300
QY      430 NCTFAHSGELEKRYRLNKKINATVTRTFPLNKGVANNVTAGNVISVIGSTETTGKI 489
DB      430 NCTFAHSGELEKRYRLNKKINATVTRTFPLNKGVANNVTAGNVISVIGSTETTGKI 489
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Db 301 NCTFAHQEELKYLBNKKINATVTPFLNKGVNNVTITAGNVISVISTETGKI 360
Qy 490 VPSTNGISNAENSVSGLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 549
Db 361 VPSTNGISNAENSVSGLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 420
Qy 550 PKPTVSNVAATSAAGSNVGTELSVPQKSSPFLTRVPYPPHSENIQYFODPRIOIPE 609
Db 421 PKPTVSNVAATSAAGSNVGTELSVPQKSSPFLTRVPYPPHSENIQYFODPRIOIPE 480
Qy 610 VPQYPTQGYPPPPYPAVACVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VPQYPTQGYPPPPYPAVACVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIRPMPYQORDIIRNSLPPMDVMHSSVYQ 729
Db 541 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIRPMPYQORDIIRNSLPPMDVMHSSVYQ 600
Qy 730 TSLRERYNSLDGYSAVACOPSPSEPTTVLPREPCGHLKTSCEBOIRRKPDQMAQYHTOK 789
Db 601 TSLRERYNSLDGYSAVACOPSPSEPTTVLPREPCGHLKTSCEBOIRRKPDQMAQYHTOK 660
Qy 790 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNVAVLMDLSDGVKRRVHLFETQRTKEEDPIIFPSGPIISKGAIS 909
Db 721 AIDSEPKDVIANSNVAVLMDLSDGVKRRVHLFETQRTKEEDPIIFPSGPIISKGAIS 780
Qy 910 RSSRTGYHTTDPVQATASQGSATKPIVSVDYVPYVAVDSRMSYNGEATSSAHYVERDR 969
Db 781 RSSRTGYHTTDPVQATASQGSATKPIVSVDYVPYVAVDSRMSYNGEATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKXSSSTGDLISLELOAKSNSLLQREANALAMQKXNSLDEGHLTLNLL 1029
Db 841 FIVTDLSGHRKXSSSTGDLISLELOAKSNSLLQREANALAMQKXNSLDEGHLTLNLL 900
Qy 1030 SKEIELRNGELOSDYEDATDTKPRDIELELSALDTPDPQSGSEIIEILDIQLGISSQ 1089
Db 901 SKEIELRNGELOSDYEDATDTKPRDIELELSALDTPDPQSGSEIIEILDIQLGISSQ 960
Qy 1090 NQOLNGMAVENGHPIVQHQKEPKQKOSLGEDHYILEBOKTILPVTSQFSGPLFVVIS 1149
Db 961 NQOLNGMAVENGHPIVQHQKEPKQKOSLGEDHYILEBOKTILPVTSQFSGPLFVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSSEKDNFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSSEKDNFLKPVANGKXVNS 1062

RESULT 10
US-60-452-680-22108
; Sequence 22108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22108
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22108

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Query Match 88.9%; Score 5525; DB 49; Length 1062;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 MORKLVTLVNCOLVEBGRVVRMARARSIGETVTELLIOHNPOLSANLMAAVRARC 189
Db 1 MORKLVTLVNCOLVEBGRVVRMARARSIGETVTELLIOHNPOLSANLMAAVRARC 60
Qy 150 QFLGPMQEBALKVLALLLEDGALSRLVLFVVQRLEPPRPAQSKTISIGHVOLLVRA 249
Db 61 QFLGPMQEBALKVLALLLEDGALSRLVLFVVQRLEPPRPAQSKTISIGHVOLLVRA 120
Qy 250 SCFKYTKRDESSLMQKKEFYSYALRREHQAQIVHIMEGLAISPOWSSLLYGDLA 309
Db 121 SCFKYTKRDESSLMQKKEFYSYALRREHQAQIVHIMEGLAISPOWSSLLYGDLA 180
Qy 310 HKSMMOSIIDKLQSPESFAKSVQELTIYVQRTGDPANLRRLPHLELANIDPNDAVSP 369
Db 181 HKSMMOSIIDKLQSPESFAKSVQELTIYVQRTGDPANLRRLPHLELANIDPNDAVSP 240
Qy 370 TWEOLENMAVAVKTVVHGLVDFIIONYSRKGHETPOPNKSKYKTSWCRDLRQGGCPRG 429
Db 241 TWEOLENMAVAVKTVVHGLVDFIIONYSRKGHETPOPNKSKYKTSWCRDLRQGGCPRG 300
Qy 430 NCTFAHQEELKYLBNKKINATVTPFLNKGVNNVTITAGNVISVISTETGKI 489
Db 301 NCTFAHQEELKYLBNKKINATVTPFLNKGVNNVTITAGNVISVISTETGKI 360
Qy 490 VPSTNGISNAENSVSGLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 549
Db 361 VPSTNGISNAENSVSGLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 420
Qy 550 PKPTVSNVAATSAAGSNVGTELSVPQKSSPFLTRVPYPPHSENIQYFODPRIOIPE 609
Db 421 PKPTVSNVAATSAAGSNVGTELSVPQKSSPFLTRVPYPPHSENIQYFODPRIOIPE 480
Qy 610 VPQYPTQGYPPPPYPAVACVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VPQYPTQGYPPPPYPAVACVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIRPMPYQORDIIRNSLPPMDVMHSSVYQ 729
Db 541 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIRPMPYQORDIIRNSLPPMDVMHSSVYQ 600
Qy 730 TSLRERYNSLDGYSAVACOPSPSEPTTVLPREPCGHLKTSCEBOIRRKPDQMAQYHTOK 789
Db 601 TSLRERYNSLDGYSAVACOPSPSEPTTVLPREPCGHLKTSCEBOIRRKPDQMAQYHTOK 660
Qy 790 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNVAVLMDLSDGVKRRVHLFETQRTKEEDPIIFPSGPIISKGAIS 909
Db 721 AIDSEPKDVIANSNVAVLMDLSDGVKRRVHLFETQRTKEEDPIIFPSGPIISKGAIS 780
Qy 910 RSSRTGYHTTDPVQATASQGSATKPIVSVDYVPYVAVDSRMSYNGEATSSAHYVERDR 969
Db 781 RSSRTGYHTTDPVQATASQGSATKPIVSVDYVPYVAVDSRMSYNGEATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKXSSSTGDLISLELOAKSNSLLQREANALAMQKXNSLDEGHLTLNLL 1029
Db 841 FIVTDLSGHRKXSSSTGDLISLELOAKSNSLLQREANALAMQKXNSLDEGHLTLNLL 900
Qy 1030 SKEIELRNGELOSDYEDATDTKPRDIELELSALDTPDPQSGSEIIEILDIQLGISSQ 1089
Db 901 SKEIELRNGELOSDYEDATDTKPRDIELELSALDTPDPQSGSEIIEILDIQLGISSQ 960
Qy 1090 NQOLNGMAVENGHPIVQHQKEPKQKOSLGEDHYILEBOKTILPVTSQFSGPLFVVIS 1149
Db 961 NQOLNGMAVENGHPIVQHQKEPKQKOSLGEDHYILEBOKTILPVTSQFSGPLFVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSSEKDNFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSSEKDNFLKPVANGKXVNS 1062

```

RESULT 11
 US-60-453-050-13598
 ; Sequence 13598, Application us/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: LUKE, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001457
 ; CURRENT APPLICATION NUMBER: US/60/453, 050
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13598
 ; LENGTH: 1062
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-60-453-050-13598

Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 MORKLTVLVNCOI VEEGRVVRAMRAARSIGERTVTELLIOHONPOOLSANLMAA VPARGC 189
 DB 1 MORKLTVLVNCOI VEEGRVVRAMRAARSIGERTVTELLIOHONPOOLSANLMAA VPARGC 60
 QY 190 OFLGRPMOBEAL KVLVLALEDGSALSRKVLV FVVOQLBRRPPOAKSTIGHVVOQLLYRA 249
 DB 61 OFLGRPMOBEAL KVLVLALEDGSALSRKVLV FVVOQLBRRPPOAKSTIGHVVOQLLYRA 120
 QY 250 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 309
 DB 121 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 180
 QY 310 HKSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLRLRPHLELLANIDNPDAVSP 369
 DB 181 HKSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLRLRPHLELLANIDNPDAVSP 240
 QY 370 TWEOLENAMAVKTVVHGVLDFIQNYSRKGHETPOQPNSKYKTSICRDLRQGGCPRGT 429
 DB 241 TWEOLENAMAVKTVVHGVLDFIQNYSRKGHETPOQPNSKYKTSICRDLRQGGCPRGT 300
 QY 430 NCTFAHSELEKYLRLNKKINATVTPPLNKGVNNVTVTAGNVISIGSTETTGKI 489
 DB 301 NCTFAHSELEKYLRLNKKINATVTPPLNKGVNNVTVTAGNVISIGSTETTGKI 360
 QY 490 VPSTNGISNAENSVSGLISRSTSTLRALETYKVGKVGANGONAAGPSADSVTEKNIGS 549
 DB 361 VPSTNGISNAENSVSGLISRSTSTLRALETYKVGKVGANGONAAGPSADSVTEKNIGS 420
 QY 550 PKTSPVNSAASAGSNVTGELNSVPOKSSPFLTVPPYPPHSENIQVFODRTOIPRE 609
 DB 421 PKTSPVNSAASAGSNVTGELNSVPOKSSPFLTVPPYPPHSENIQVFODRTOIPRE 480
 QY 610 VFQYQOTGYPPPTVPAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRRMNS 669
 DB 481 VFQYQOTGYPPPTVPAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRRMNS 540
 QY 670 SFYQPPPPQYGPVPVPSGMYAPVYDSRRIMRPMYQORDDITRSNLSRPMVMHSSVYQ 729
 DB 541 SFYQPPPPQYGPVPVPSGMYAPVYDSRRIMRPMYQORDDITRSNLSRPMVMHSSVYQ 600
 QY 730 TSLREYVNSLDGYSAQCPSPSPRTTVLPRPCGHLKTSCEQJRRKPDQAOYHTOK 789
 DB 601 TSLREYVNSLDGYSAQCPSPSPRTTVLPRPCGHLKTSCEQJRRKPDQAOYHTOK 660
 QY 790 APLVSLTLVATQSPRPSPPLFVDFRADFSSESVGTKFEEDHLSHYSPWSCGTTIGSCIN 849
 DB 661 APLVSLTLVATQSPRPSPPLFVDFRADFSSESVGTKFEEDHLSHYSPWSCGTTIGSCIN 720

QY 850 AIDSEPKVIANSNAVLMDLSDGVKRRVHLPETQRTKEEDPIIFPSDGIISKMGATIS 909
 DB 721 AIDSEPKVIANSNAVLMDLSDGVKRRVHLPETQRTKEEDPIIFPSDGIISKMGATIS 780
 QY 910 RSSRGTGHTTDPVOATASOGSATKPIISVSDYPPYVNAVDSRWSSYGENATSSAHYERDR 969
 DB 781 RSSRGTGHTTDPVOATASOGSATKPIISVSDYPPYVNAVDSRWSSYGENATSSAHYERDR 840
 QY 970 FIVTDLGSRKHISSTGDLISLELOAKSN\$LLLOREANALAMQKNSLDEGRHLTLNLL 1029
 DB 841 FIVTDLGSRKHISSTGDLISLELOAKSN\$LLLOREANALAMQKNSLDEGRHLTLNLL 900
 QY 1030 SKEIELRNGELOS DTEADTDPRDIELELSALDTPDQSGSEPIETLIDIQLGIS\$Q 1069
 DB 901 SKEIELRNGELOS DTEADTDPRDIELELSALDTPDQSGSEPIETLIDIQLGIS\$Q 960
 QY 1090 NQOLINGMAVENGHAPVOHQKPEPKQKOSLGEDHVIIEOKTILPVTSCF\$QPLPV\$IS 1149
 DB 961 NQOLINGMAVENGHAPVOHQKPEPKQKOSLGEDHVIIEOKTILPVTSCF\$QPLPV\$IS 1020
 QY 1150 NASCLPITTSV\$AGNLIILKTHVMS\$EDKNDPLKPVANGKXVNS 1191
 DB 1021 NASCLPITTSV\$AGNLIILKTHVMS\$EDKNDPLKPVANGKXVNS 1062

RESULT 12
 US-60-453-135-13598
 ; Sequence 13598, Application us/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: TAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001456
 ; CURRENT APPLICATION NUMBER: US/60/453, 135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13598
 ; LENGTH: 1062
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-60-453-135-13598

Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 MORKLTVLVNCOI VEEGRVVRAMRAARSIGERTVTELLIOHONPOOLSANLMAA VPARGC 189
 DB 1 MORKLTVLVNCOI VEEGRVVRAMRAARSIGERTVTELLIOHONPOOLSANLMAA VPARGC 60
 QY 190 OFLGRPMOBEAL KVLVLALEDGSALSRKVLV FVVOQLBRRPPOAKSTIGHVVOQLLYRA 249
 DB 61 OFLGRPMOBEAL KVLVLALEDGSALSRKVLV FVVOQLBRRPPOAKSTIGHVVOQLLYRA 120
 QY 250 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 309
 DB 121 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 180
 QY 310 HKSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLRLRPHLELLANIDNPDAVSP 369
 DB 181 HKSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLRLRPHLELLANIDNPDAVSP 240
 QY 370 TWEOLENAMAVKTVVHGVLDFIQNYSRKGHETPOQPNSKYKTSICRDLRQGGCPRGT 429
 DB 241 TWEOLENAMAVKTVVHGVLDFIQNYSRKGHETPOQPNSKYKTSICRDLRQGGCPRGT 300
 QY 430 NCTFAHSELEKYLRLNKKINATVTPPLNKGVNNVTVTAGNVISIGSTETTGKI 489
 DB 301 NCTFAHSELEKYLRLNKKINATVTPPLNKGVNNVTVTAGNVISIGSTETTGKI 360
 QY 490 VPSTNGISNAENSVSGLISRSTSTLRALETYKVGKVGANGONAAGPSADSVTEKNIGS 549

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Db 361 VSTNGISNAENSVQSLISRSTDSLRALETYKXVKGVANGQNAAGPADSVTEKIGS 420
Qy 550 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFODPRTOIPE 609
Db 421 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFODPRTOIPE 480
Qy 610 VQYQPTGYPPPPYPPVAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VQYQPTGYPPPPYPPVAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPOYPGVPPVPBGMYAPVYDSRRIMRPMYQBDIIIRNSLPPMDVHSSVYQ 729
Db 541 SPYQPPPOYPGVPPVPBGMYAPVYDSRRIMRPMYQBDIIIRNSLPPMDVHSSVYQ 600
Qy 730 TSLREKYNLSDGYSAACQPPSEPRITVLPREPCHLKTSCBEOJRRKPDQAOYHTQK 789
Db 601 TSLREKYNLSDGYSAACQPPSEPRITVLPREPCHLKTSCBEOJRRKPDQAOYHTQK 660
Qy 790 APLVSTLPLVATQSPTRPSPPLFVSVDPRADFSESVSCTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPTRPSPPLFVSVDPRADFSESVSCTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNAVLMDLSDGDKRVYHLEFQRTKEBDPIIPFSDGPIISKMGALS 909
Db 721 AIDSEPKDVIANSNAVLMDLSDGDKRVYHLEFQRTKEBDPIIPFSDGPIISKMGALS 780
Qy 910 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 969
Db 781 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQOKNNSLDEGHLLTLNLL 1029
Db 841 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQOKNNSLDEGHLLTLNLL 900
Qy 1030 SKEIELRNELOSDYEDATDTKPRDIELEISALDTPDQSGSEPIEBIILDIQLGISQ 1089
Db 901 SKEIELRNELOSDYEDATDTKPRDIELEISALDTPDQSGSEPIEBIILDIQLGISQ 960
Qy 1090 NQOLNGMAVENHPIVQOHQKPPKOKKOSLGEDHYILEOKTILVTSCFSQPLVVIS 1149
Db 961 NQOLNGMAVENHPIVQOHQKPPKOKKOSLGEDHYILEOKTILVTSCFSQPLVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSBDKNDFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSBDKNDFLKPVANGKXVNS 1062

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RESULT 13
US-60-466-412-13598
; Sequence 13598, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/60/466,412
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13598
; LENGTH: 1062
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-466-412-13598

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Query Match 88.9%; Score 5525; DB 49; Length 1062;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 130 MQRKLTVLNQCULVEEGRVRAARAASLGERTVTEILLOHONPOOLSANLMAAVRARGC 189

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Db 1 MQRKLTVLNQCULVEEGRVRAARAASLGERTVTEILLOHONPOOLSANLMAAVRARGC 60
Qy 190 QFLGPMOBEALKVLALLLEDSSALSRKVLVLFVVOQLBPPRPOASKTISGHVOLLYRA 249
Db 61 QFLGPMOBEALKVLALLLEDSSALSRKVLVLFVVOQLBPPRPOASKTISGHVOLLYRA 120
Qy 250 SCFKYTKRDEDSLSMLQKEFRSYEALRREHDAQIVHIMEAGLRISPEOWSSLYGDLA 309
Db 121 SCFKYTKRDEDSLSMLQKEFRSYEALRREHDAQIVHIMEAGLRISPEOWSSLYGDLA 180
Qy 310 HXSHMOIIDKLOQSPESFAKSVQELTIVLQRTGDPANLRLRPHLELANIDPNPAVSP 369
Db 181 HXSHMOIIDKLOQSPESFAKSVQELTIVLQRTGDPANLRLRPHLELANIDPNPAVSP 240
Qy 370 TWEOLENAMVAKYTVHGLVDFIQNSYRKGHTTPOPOPNSKTKTSMCRDLROOGGCPRT 429
Db 241 TWEOLENAMVAKYTVHGLVDFIQNSYRKGHTTPOPOPNSKTKTSMCRDLROOGGCPRT 300
Qy 430 NCTFAHSGEELBKRYLRNKKINATVTFPLNKGVMNTVTYTAGNVISIGSTETTKI 489
Db 301 NCTFAHSGEELBKRYLRNKKINATVTFPLNKGVMNTVTYTAGNVISIGSTETTKI 360
Qy 490 VSTNGISNAENSVQSLISRSTDSLRALETYKXVKGVANGQNAAGPADSVTEKIGS 549
Db 361 VSTNGISNAENSVQSLISRSTDSLRALETYKXVKGVANGQNAAGPADSVTEKIGS 420
Qy 550 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFODPRTOIPE 609
Db 421 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFODPRTOIPE 480
Qy 610 VQYQPTGYPPPPYPPVAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VQYQPTGYPPPPYPPVAGVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPOYPGVPPVPBGMYAPVYDSRRIMRPMYQBDIIIRNSLPPMDVHSSVYQ 729
Db 541 SPYQPPPOYPGVPPVPBGMYAPVYDSRRIMRPMYQBDIIIRNSLPPMDVHSSVYQ 600
Qy 730 TSLREKYNLSDGYSAACQPPSEPRITVLPREPCHLKTSCBEOJRRKPDQAOYHTQK 789
Db 601 TSLREKYNLSDGYSAACQPPSEPRITVLPREPCHLKTSCBEOJRRKPDQAOYHTQK 660
Qy 790 APLVSTLPLVATQSPTRPSPPLFVSVDPRADFSESVSCTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPTRPSPPLFVSVDPRADFSESVSCTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNAVLMDLSDGDKRVYHLEFQRTKEBDPIIPFSDGPIISKMGALS 909
Db 721 AIDSEPKDVIANSNAVLMDLSDGDKRVYHLEFQRTKEBDPIIPFSDGPIISKMGALS 780
Qy 910 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 969
Db 781 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQOKNNSLDEGHLLTLNLL 1029
Db 841 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQOKNNSLDEGHLLTLNLL 900
Qy 1030 SKEIELRNELOSDYEDATDTKPRDIELEISALDTPDQSGSEPIEBIILDIQLGISQ 1089
Db 901 SKEIELRNELOSDYEDATDTKPRDIELEISALDTPDQSGSEPIEBIILDIQLGISQ 960
Qy 1090 NQOLNGMAVENHPIVQOHQKPPKOKKOSLGEDHYILEOKTILVTSCFSQPLVVIS 1149
Db 961 NQOLNGMAVENHPIVQOHQKPPKOKKOSLGEDHYILEOKTILVTSCFSQPLVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSBDKNDFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSBDKNDFLKPVANGKXVNS 1062

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RESULT 14
US-10-485-225-8

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; Sequence 8, Application US/10485225
; GENERAL INFORMATION:
; APPLICANT: Greener, Tsvika
; APPLICANT: Moskowitz, Haim
; APPLICANT: Reies, Yuval
; APPLICANT: Aliroy, Irit
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: MODULATION OF VIRAL MATURATION
; FILE REFERENCE: PROL-P02-001
; CURRENT APPLICATION NUMBER: US/10/485,225
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/345,846
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-225-8

Query Match      88.2%; Score 5483; DB 34; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPVQAQWTEFLSCPCVNEFDENVHKPISLGSHTVCTCKLHKRKAQPFQTAINTD 60
Db 1 MPVQAQWTEFLSCPCVNEFDENVHKPISLGSHTVCTCKLHKRKAQPFQTAINTD 60
Qy 61 IDLVPNALLQLVGAQVDPHOSIKLSNGENKHYEVAKKCYEDLALYKPLSGKGVAS 120
Db 61 IDLVPNALLQLVGAQVDPHOSIKLSNGENKHYEVAKKCYEDLALYKPLSGKGVAS 120
Qy 121 INOSLSPMOKRLTVLVNCOIVEEGRVAMRAARSIGERTVTELLIOHONPOOLSAVL 180
Db 121 INOSLSPMOKRLTVLVNCOIVEEGRVAMRAARSIGERTVTELLIOHONPOOLSAVL 180
Qy 121 INOSLSPMOKRLTVLVNCOIVEEGRVAMRAARSIGERTVTELLIOHONPOOLSAVL 180
Db 121 INOSLSPMOKRLTVLVNCOIVEEGRVAMRAARSIGERTVTELLIOHONPOOLSAVL 180
Qy 181 WAAVBARCGCFGLPAMOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIG 240
Db 181 WAAVBARCGCFGLPAMOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIG 240
Qy 181 WAAVBARCGCFGLPAMOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIG 240
Db 181 WAAVBARCGCFGLPAMOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIG 240
Qy 241 HVVOLLYPASCFKVTTRDESSLMOLKEFRSYEALRREHDAQIVHIAEAGLRISPEOW 300
Db 241 HVVOLLYPASCFKVTTRDESSLMOLKEFRSYEALRREHDAQIVHIAEAGLRISPEOW 300
Qy 301 SSLLYGDLAKHSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLNLRPHLELANI 360
Db 301 SSLLYGDLAKHSHMOSIIDKLOSPESFAKSVQELTIVLQRTGDPANLNLRPHLELANI 360
Qy 361 DENPDVSPFTWOLENAMVAVKTIVHGLVDFIONYSRKSHETPOPQNSKYTSMCRDLR 420
Db 361 DENPDVSPFTWOLENAMVAVKTIVHGLVDFIONYSRKSHETPOPQNSKYTSMCRDLR 420
Qy 421 OQGGCPRGNTCTFAHSOELEKYLRLNKKINATVTFPLLNKRVGNVNTTTAGNVISVI 480
Db 421 OQGGCPRGNTCTFAHSOELEKYLRLNKKINATVTFPLLNKRVGNVNTTTAGNVISVI 480
Qy 481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSSTLPALETVKVGVGANGONAGPSAD 540
Db 481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSSTLPALETVKVGVGANGONAGPSAD 540
Qy 541 SYTENKIGSPKTPVSNVATAGPSNVGTIELNSVPQKSPFLTRPVVPHPHSENIQYFQ 600
Db 541 SYTENKIGSPKTPVSNVATAGPSNVGTIELNSVPQKSPFLTRPVVPHPHSENIQYFQ 600
Qy 601 DPTROIPEFVPOYPOTGIYPPPTTVAGYAPCVPRFVRSNNYPESSGLPPASMPYADHYST 660
Db 601 DPTROIPEFVPOYPOTGIYPPPTTVAGYAPCVPRFVRSNNYPESSGLPPASMPYADHYST 660
Qy 661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
Db 661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
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Db 661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
Qy 721 DVMSSVYQTSILREYRNSLDGIYVACOPPSPEPRTTVLPREPCHLTKSCBEOIRKRD 780
Db 721 DVMSSVYQTSILREYRNSLDGIYVACOPPSPEPRTTVLPREPCHLTKSCBEOIRKRD 780
Qy 781 OMAQYHTOKAPLVSTLPAVATOSPFPSPPLFVDRADSESVSGTKFEEDHLSHSPMS 840
Db 781 OMAQYHTOKAPLVSTLPAVATOSPFPSPPLFVDRADSESVSGTKFEEDHLSHSPMS 840
Qy 841 CGTIGSCINADSEKEDVYANSNAVIMDLSDGVKRRVHLFETORTKEDEPIIPSDGP 900
Db 841 CGTIGSCINADSEKEDVYANSNAVIMDLSDGVKRRVHLFETORTKEDEPIIPSDGP 900
Qy 901 IISKWGAISRSGRTGHTTDPVQATASQCATKPIVSVDYVYVNAVDSRMSYNGEATS 960
Db 901 IISKWGAISRSGRTGHTTDPVQATASQCATKPIVSVDYVYVNAVDSRMSYNGEATS 960
Qy 961 SAHYVERDFTVTDLSGHRKHSSTGDLSTLELOAKSNSLLQREANALAMOOKNSLDE 1020
Db 961 SAHYVERDFTVTDLSGHRKHSSTGDLSTLELOAKSNSLLQREANALAMOOKNSLDE 1020
Qy 1021 GRHLTLNLISKEIELRNGELQSDYTEDA 1048
Db 1021 GRHLTLNLISKEIELRNGELQSDYTEDA 1048

RESULT 15
US-09-488-725A-3499
; Sequence 3499, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseg Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3495
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3499

Query Match      71.1%; Score 4416; DB 24; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 844; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 196 MOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIGHVVOLLYPASCFKXT 255
Db 1 MOEALKLVLALDGSALSRKVLVLFVVOQLBEPFPOASTSIGHVVOLLYPASCFKXT 255
Qy 256 KRDESSLMOLKEFRSYEALRREHDAQIVHIAEAGLRISPEOWSSLLYGLAKHSHNQ 315
Db 256 KRDESSLMOLKEFRSYEALRREHDAQIVHIAEAGLRISPEOWSSLLYGLAKHSHNQ 315
Qy 316 SIIDKLOSPESFAKSVQELTIVLQRTGDPANLNLRPHLELANIDPNDVSPFTWOLE 375
Db 316 SIIDKLOSPESFAKSVQELTIVLQRTGDPANLNLRPHLELANIDPNDVSPFTWOLE 375
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Db 121 SIIIDKQSPESPAKSVQBELTIVLQRTGDBANLRLRPHLELLANIDPNDAVSPTEQLE 180
QY 376 NAMVAVKTVVHGLVDFIQNYSRKHGHTPPQPNNSKYKTSMCRDLROQGGCPRGINTCFMH 435
Db 181 NAMVAVKTVVHGLVDFIQNYSRKHGHTPPQPNNSKYKTSMCRDLROQGGCPRGINTCFMH 240
QY 436 SOEELKRYLRNKKINATVTRFPLLNKVGNNVTVTAGNVISVIGSTETTKIVPSTNG 495
Db 241 SOEELKRYLRNKKINATVTRFPLLNKVGNNVTVTAGNVISVIGSTETTKIVPSTNG 300
QY 496 ISNAENSVSQILSRSTDSLRLALETVKKVKGANGQNAAGPSADSVTENKIGSPKTPV 555
Db 301 ISNAENSVSQILSRSTDSLRLALETVKKVKGANGQNAAGPSADSVTENKIGSPKTPV 360
QY 556 SNVAATISAGPSNVGTBLNSVPQKSSPFLTRVPVYPHSENIOYFQDPRTQIPEVPQYPO 615
Db 361 SNVAATISAGPSNVGTBLNSVPQKSSPFLTRVPVYPHSENIOYFQDPRTQIPEVPQYPO 420
QY 616 TGYPPPTVPAGVAPCVPRFVRSNNVPSSLPASMPYADHYSTPSPRDRMNSPYQPP 675
Db 421 TGYPPPTVPAGVAPCVPRFVRSNNVPSSLPASMPYADHYSTPSPRDRMNSPYQPP 480
QY 676 PPQYGPVPVPVPSGMVAPYDSRRIRWPRMYORDIIRSNLSLPPMDVMHSSVYQTSLRER 735
Db 481 PPQYGPVPVPVPSGMVAPYDSRRIRWPRMYORDIIRSNLSLPPMDVMHSSVYQTSLRER 540
QY 736 YNSLDGYSVACQPPSEPRRTVPLPREPCGHLKTSCEQIRRKPDQWAOYHTQKAPLVSS 795
Db 541 YNSLDGYSVACQPPSEPRRTVPLPREPCGHLKTSCEQIRRKPDQWAOYHTQKAPLVSS 600
QY 796 TLPVATQSPPTPSPPLFSVDFRADFSSEVSQTKFEEDHLSHYSPWSCGTTGSCINAIIDSEP 855
Db 601 TLPVATQSPPTPSPPLFSVDFRADFSSEVSQTKFEEDHLSHYSPWSCGTTGSCINAIIDSEP 660
QY 856 KQVIANSNAVLMDLDSGDVYKRRVHLFETQRTKEEDPIIPFSDGPIISKWGAISRSSRTG 915
Db 661 KQVIANSNAVLMDLDSGDVYKRRVHLFETQRTKEEDPIIPFSDGPIISKWGAISRSSRTG 720
QY 916 YHTTDPVQATASQGSATKPIISVSDVYPYNAVDSRWSYGNENTSSAHYVERDRFTVTDL 975
Db 721 YHTTDPVQATASQGSATKPIISVSDVYPYNAVDSRWSYGNENTSSAHYVERDRFTVTDL 780
QY 976 SGHRKHSSTGDDLSTLELQAKSNSLLQREANALAMQKWNLSDEGRHLTLNLSKEIEL 1035
Db 781 SGHRKHSSTGDDLSTLELQAKSNSLLQREANALAMQKWNLSDEGRHLTLNLSKEIEL 840
QY 1036 RNGELQ 1041
Db 841 RNGEVK 846
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